



# **STIC Search Report**

## **Biotech-Chem Library**

STIC Database Tracking Number: 99797

TO: Holly Schnizer  
Location: CM1/9E09/9B01  
Monday, July 28, 2003  
Art Unit: 1653  
Phone: 305-3722  
Serial Number: 09 / 302239

From: Jan Delaval  
Location: Biotech-Chem Library  
CM1-1E07  
Phone: 308-4498

[jan.delaval@uspto.gov](mailto:jan.delaval@uspto.gov)

### Search Notes

Jan Delaval  
Reference Librarian  
Biotechnology & Chemical Library  
CM1 1E07 - 703-308-4498  
[jan.delaval@uspto.gov](mailto:jan.delaval@uspto.gov)

**0000 PAGE BLANK (USPTO)**

; Entered [jdelaval 28-Jul-03 11:42]  
SEQ3  
ANAFIXXLRQGSIXRXCKXXQCSFXAXXIFKDAKRTKLPWISY1

; Entered [jdelaval 28-Jul-03 11:43]  
SEQ4  
ANGFLXXLRQGSIXRXCKXXICSPXAXXIFRNXXRTROFWVS1

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 28, 2003, 12:21:05 ; Search time 25 Seconds  
(without alignments)  
169.257 Million cell updates/sec

Title: SEQ3  
Perfect score: 190  
Sequence: 1 ANAFIXLRGSLRXCKXX.....XXARXIFDXARFLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR\_76:\*  
2: pir1:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164	86.3	466	1 KFHU7	coagulation factor
2	130	68.4	443	2 I46932	coagulation factor
3	115	60.5	407	1 KFB07	coagulation factor
4	107	56.3	492	1 EXBO	coagulation factor
5	104	54.7	488	1 EXHU	coagulation factor
6	101	53.2	461	1 JX0210	protein C (activat
7	100	52.6	461	1 S18994	protein C (activat
8	98	51.6	482	1 EXRT	coagulation factor
9	97	51.1	475	1 EXCH	coagulation factor
10	96	50.5	456	1 KXBO	coagulation factor
11	88	46.3	461	1 KFHU	coagulation factor
12	87	45.8	416	1 KFB0	coagulation factor
13	86	45.3	461	1 KXHU	coagulation factor
14	85	44.7	622	1 TBHU	protein C (activat
15	81	42.6	617	2 S10511	thrombin (EC 3.4.2
16	81	42.6	618	2 A35827	thrombin (EC 3.4.2
17	79	41.6	452	1 A30351	coagulation factor
18	79	41.6	459	2 J00419	coagulation factor
19	75	39.5	642	2 S53433	plasma protein S p
20	70	36.8	642	2 S53434	plasma protein S p
21	70	36.8	676	1 KXHU	plasma protein S p
22	68	35.8	675	1 KXBO	plasma protein S p
23	66	34.7	396	1 KXBO	plasma protein S -
24	66	34.7	396	2 S38819	thrombin (EC 3.4.2
25	65	34.2	625	1 TBBO	plasma protein S -
26	65	34.2	675	1 KXRTS	plasma protein S p
27	63.5	33.4	576	2 G96763	probable MAP kinase
28	61	32.1	422	1 KXHU	plasma protein Z p
29	61	32.1	673	2 A48089	growth arrest-spec

30	59	31.1	674	2 I55476	growth potentiating
31	59	31.1	678	2 B48089	growth arrest-spec
32	58	30.5	675	1 KXMS	plasma protein S p
33	57.5	30.3	594	2 D84859	probable MAP kinase
34	57.5	30.3	603	2 C96575	probable MAP kinase
35	46.5	24.5	161	2 F82637	conserved hypotet
36	45.5	23.9	516	2 H84424	probable MAP kinase
37	45	23.7	879	2 S55864	hypothetical prote
38	44.5	23.4	455	2 C83494	probable 2-isoprop
39	44	23.2	211	2 D96996	uncharacterized lo
40	43.5	22.9	367	2 B56598	endothelial kinase
41	43.5	22.9	385	2 T15221	hypothetical prote
42	43.5	22.9	1298	2 A48999	protein-tyrosine k
43	43.5	22.9	1363	2 I58375	protein-tyrosine k
44	43.5	22.9	1379	2 J04954	vascular endotheli
45	43	22.6	370	2 E83518	probable acyl-CoA

#### ALIGNMENTS

RESULT 1  
KFB07  
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human  
C/Species: Homo sapiens (man)  
C/Date: 19-May-1989 #sequence revision 19-May-1994 #text\_change 08-Dec-2000  
C/Accession: A28322, A28819, A31186, B31186, S63524  
R/O'Hara, F.J.; Grant, F.J.; Halldeman, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; Murr  
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987  
A/Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depend  
A/Reference number: A28322; MUID:87260948; PMID:3037537  
A/Accession: A28322  
A/Molecule type: DNA  
A/Residues: 1-466 <OHA>  
A/Cross-references: GB:002933; NID:9180333; PIDN:AAA51983.1; PID:9180334  
R/Hagen, F.S.; Gray, C.L.; O'Hara, F.J.; Grant, F.J.; Saarl, G.C.; Woodbury, R.G.; Hart, C  
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986  
A/Title: Characterization of a cDNA coding for human factor VII.  
A/Reference number: A23819; MUID:86205965; PMID:3346420  
A/Accession: A23819  
A/Molecule type: mRNA  
A/Residues: 1-466 <HAG>  
A/Cross-references: GB:M13232; NID:91827799; PIDN:AAA8040.1; PID:9182801  
R/Thim, L.; Bjorn, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.  
Biochemistry 27, 7785-7793, 1988  
A/Title: Amino acid sequence and posttranslational modifications of human factor VII-a f  
A/Reference number: A90539; MUID:89088153; PMID:3264725  
A/Accession: A31186  
A/Molecule type: protein  
A/Residues: 61-212 <THI>  
A/Accession: B31186  
A/Molecule type: protein  
A/Residues: 213-466 <TH2>  
R/Bjorn, S.; Foster, D.C.; Thim, L.; Wlberg, F.C.; Christensen, M.; Komiyama, Y.; Peder  
J. Biol. Chem. 266, 11051-11057, 1991  
A/Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations a  
A/Reference number: A40529; MUID:91250411; PMID:1904059  
R/Persson, E.; Petersen, L.C.  
Eur. J. Biochem. 234, 293-300, 1995  
A/Title: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carbox  
A/Reference number: S63524; MUID:96096752; PMID:8529655  
A/Accession: S63524  
A/Molecule type: protein  
A/Residues: 61-65;99-103;105-109;213-217;308-312 <PER>  
C/Genetics:  
A/Gene: GDB:F7  
A/Cross-references: GDB:119897; OMIM:227500  
A/Map position: 13q34-13q34  
A/Intons: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1  
C/Function:  
A/Description: catalyzes the proteolytic activation of coagulation factor X in the presen  
coagulation factor IX in the presence of calcium and tissue factor

A:Pathway: blood coagulation extrinsic pathway  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-60/Domain: propeptide #status predicted <PRO>  
F:45-104/Domain: Gla domain homology <Gla>  
F:61-212/Product: coagulation factor VIIa light chain #status experimental <MA1>  
F:110-141/Domain: EGF homology <EG1>  
F:151-187/Domain: EGF homology <EG2>  
F:213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>  
F:213-447/Domain: trypsin homology <TRY>  
F:166-67,74,76,79,80,85,86,89,95/Modified site: gamma-carboxylglutamic acid (Glu) #status  
F:77-82,110-121,115-130,132-141,151-162,156-172,174-187,195-322,219-224,238-254,370-389,  
F:112,120/Binding site: carbohydrate (Ser) (covalent) #status experimental  
F:123/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent  
F:205,382/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:212-213/Cleavage site: Arg-1le (coagulation factor X) #status experimental  
F:253,302,404/Active site: His, Asp, Ser #status predicted  
F:350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match 86.3%; Score 164; DB 1; Length 466;  
Best Local Similarity 75.0%; Pred. No. 2.8e-20;  
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRQGSLLKRXCKXXQCSFXXARXIFPDARTKLFWISY 44  
Db 61 ANAFLEELRPGSLERECKEELCSFEAREIRFDARTKLFWISY 104

RESULT 2  
146932  
coagulation factor VII - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 12-Feb-1999  
C:Accession: I46932  
A:Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII  
A:Reference number: I46933; MUID:93190306; PMID:8383365  
A:Accession: I46932  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-443 <BRO>  
A:Cross-references: GB:S56300; NID:9266294; PID:9266295  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
F:24-83/Domain: Gla domain homology <Gla>  
F:89-120/Domain: EGF homology <EG1>  
F:130-166/Domain: EGF homology <EG2>  
F:192-425/Domain: trypsin homology <TRY>

Query Match 68.4%; Score 130; DB 2; Length 443;  
Best Local Similarity 56.8%; Pred. No. 2e-14; Indels 15; Gaps 0;  
Matches 25; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRQGSLLKRXCKXXQCSFXXARXIFPDARTKLFWISY 44  
Db 40 ANSFLEELRPGSLERECKEELCSFEAREIRFDARTKLFWISY 83

RESULT 3  
KFB07  
coagulation factor VIIa (BC 3.4.21.21) - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 21-May-1990 #sequence\_revision 23-Mar-1995 #text\_change 16-Jul-1999  
C:Accession: A31979; C20274  
R:Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.  
J. Biol. Chem. 263, 14868-14877, 1988  
A:Title: Bovine factor VII. Its purification and complete amino acid sequence.  
A:Reference number: A31979; MUID:89008362; PMID:3045954  
A:Accession: A31979  
A:Molecule type: protein  
A:Residues: 1-407 <TAK>  
R:McMullen, B.W.; Fujikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
A:Reference number: A20274; MUID:83308813; PMID:6688526  
A:Accession: C20274  
A:Molecule type: protein  
A:Residues: 58-62, 'X', 64-68 <MCN>  
A>Note: The residue designated 'X' was determined to be hydroxyaspartic acid  
R:Haese, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Suenoshi, T.; Miyata, T.; Iwanaga,  
J. Biochem. 104, 867-868, 1988  
A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag  
A:Reference number: A44556; MUID:89213999; PMID:3149637  
A:Contents: annotation  
A>Note: structure and location of covalently bound carbohydrate  
C:Function:  
A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese  
gulation factor IX in the presence of calcium and tissue factor  
A:Pathway: blood coagulation extrinsic pathway  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate  
F:1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>  
F:1-44/Domain: Gla domain homology (fragment) <Gla>  
F:50-81/Domain: EGF homology <EG1>  
F:91-127/Domain: EGF homology <EG2>  
F:153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>  
F:153-387/Domain: trypsin homology <TRY>  
F:6,7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxylglutamic acid (Glu) #status  
F:17-22,50-61,55-70,72-81,91-102,96-112,114-127,135-262,159-164,178-194,310-329,340-368/  
F:52/Binding site: carbohydrate (Ser) (covalent) #status experimental  
F:63/Modified site: erythro-beta-hydroxyaspartic acid (Asp) (partial) #status experiment  
F:145,203/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:152-153/Cleavage site: Arg-1le (coagulation factor X) #status experimental  
F:193,242,344/Active site: His, Asp, Ser #status predicted  
F:290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 60.5%; Score 115; DB 1; Length 407;  
Best Local Similarity 50.0%; Pred. No. 7.1e-12;  
Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRQGSLLKRXCKXXQCSFXXARXIFPDARTKLFWISY 44  
Db 1 ANGFLEELRPGSLERECKEELCSFEAREIRFDARTKLFWISY 44

RESULT 4  
EXBO  
coagulation factor Xa (EC 3.4.21.6) precursor - bovine  
N:Alternate names: Stuart factor  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 24-Apr-1984 #sequence\_revision 17-Mar-1987 #text\_change 16-Jul-1999  
C:Accession: A22867; A14997; A12030; A34412; S39414; A00525  
R:Fung, M.R.; Campbell, R.M.; MacGillivray, T.A.  
Nucleic Acids Res. 12, 4481-4492, 1984  
A:Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a  
A:Reference number: A22867; MUID:84247315; PMID:6330671  
A:Accession: A22867  
A:Molecule type: mRNA  
A:Residues: 1-487 <FUN>  
A:Cross-references: GB:X00673; NID:g192; PID:CAA23286.1; PID:g193  
R:Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.  
Biochemistry 19, 659-667, 1980  
A:Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).  
A:Reference number: A14997; MUID:80130563; PMID:6766735  
A:Accession: A14997  
A:Molecule type: protein  
A:Residues: 41-102, 'N', 104-180 <ENF>  
R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co  
A:Reference number: A20274; MUID:83308813; PMID:6688526  
A:Contents: annotation; revision to residue 103  
R:Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.  
Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975  
A:Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.

A:Reference: number: A12030; MUID:76053069; PMID:1059093  
A:Accession: A12030  
A:Molecule type: protein  
A:Residues: 183-292,294-295, 'GDE',299-334,336-348, 'AE',351-354,356-441, 'GRK',446-492 <TR>  
A:Note: carboxydic binding sites and disulfide bonds were determined  
J:Person: E.; Selandier, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.  
J: Biol. Chem. 264, 16897-16904, 1989  
A:Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal  
A:Reference number: A34412; MUID:89380326; PMID:2789221  
A:Accession: A34412  
A:Molecule type: protein  
A:Residues: 85-126 <PER>  
A:Note: beta-hydroxyaspartic acid site  
R:Inoue, K.; Morita, T.  
Eur. J. Biochem. 218, 153-163, 1993  
A:Title: Identification of O-linked oligosaccharide chains in the activation peptides of  
A:Reference number: S39414; MUID:94062825; PMID:8243461  
A:Accession: S39414  
A:Molecule type: protein  
A:Residues: 183-196,199-209,216-233 <INO>  
A:Note: carboxydic binding sites  
R:Tilani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; D  
Biochemistry 11, 4899-4903, 1972  
A:Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammalian  
A:Reference number: A12453; MUID:73053314; PMID:4264286  
A:Contents: annotation; active site  
R:Fujikawa, K.; Tilani, K.; Davie, E.W.  
Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975  
A:Title: Activation of bovine factor X (Stuart factor): conversion of factor Xa1pha to  
A:Reference number: A13504; MUID:76053121; PMID:1059122  
A:Contents: annotation; activation  
R:Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.  
J. Biol. Chem. 259, 5705-5710, 1984  
A:Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic  
A:Reference number: A38024; MUID:984185716; PMID:6546930  
A:Contents: annotation; calcium binding  
R:Morita, T.; Jackson, C.M.  
J. Biol. Chem. 261, 4008-4014, 1986  
A:Reference number: A38025; MUID:86140210; PMID:3949800  
A:Contents: annotation; sulfate binding  
C:Comment: Factor Xa converts prothrombin to thrombin during blood clotting.  
C:Comment: The two chains are formed from a single-chain precursor by the excision of two  
C:Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), C  
activation.  
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with stromelytin  
C:Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin  
C:Genetics:  
A:Gene: F10  
A:Map position: 13q34  
C:Function:  
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
A:Pathway: blood coagulation  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutamat  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:16-40/Domain: propeptide #status predicted <PRO>  
F:25-84/Domain: Gla domain homology <Gla>  
F:41-180/Product: coagulation factor X light chain #status experimental <LCH>  
F:190-121/Domain: EGF homology <EGF>  
F:129-164/Domain: EGF homology <EG2>  
F:183-452/Product: coagulation factor X heavy chain #status experimental <HCH>  
F:183-233/Domain: activation peptide #status experimental <AP>  
F:234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>  
F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #  
F:234-461/Domain: trypsin homology <TRY>  
F:57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-341/Disulfide bonds: #status  
F:100/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
F:200/Binding site: sulfite (Tyr) (covalent) (partial) #status experimental  
F:208,485/Binding site: carboxylate (Thr) (covalent) #status experimental  
F:218/Binding site: carboxylate (Asn) (covalent) #status experimental  
F:220-223/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #sta  
F:220-245,260-276,389-403,413-442/Disulfide bonds: #status experimental  
F:275,321,418/Active site: His, Asp, Ser #status predicted

Query Match Similarity 56.3%; Score 107; DB 1; length 492;  
Best Local Similarity 45.5%; Pred. No. 2e-10;  
Matches 20; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

RESULT 5

EXNHU  
coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human

N.Alternate names: Stuart factor  
C.Species: Homo sapiens (man)  
C.Date: 15-Nov-1984 #sequence\_revision 02-May-1994 #next change 08-Dec-2000  
C.Accession: A24478; J00917; A42485; A25853; A22208; A21284; A20362; S39415; I54051; A00  
R.Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.  
Biochemistry 25, 5098-5102, 1986  
A.Title: Gene for human Factor X: a blood coagulation factor whose gene organization is  
A.Reference number: A24478; PMID:87026600; PMID:3768336  
A.Accession: A24478

A.Molecule type: DNA  
A.Residues: 1-488 <LEX>  
A.Cross-references: GB:I29433; GB:M14327; NID:9459809; PIDN:AAA52764.1; PID:g182831  
R.Meisler, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.T.; Church, W.R.  
Gene 99, 291-294, 1991  
A>Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coagulation factor X  
A.Reference number: J00917; PMID:91216473; PMID:1502434  
A.Accession: J00917

A.Molecule type: mRNA  
A.Residues: 1-488 <MES>  
A.Cross-references: GB:M57285; NID:9182389; PIDN:AAA52421.1; PID:g182390  
R.Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.  
J Biol. Chem. 267, 7395-7401, 1992  
A>Title: Liver-specific expression of the gene coding for human factor X, a blood coagul  
A.Reference number: A42485; PMID:92218390; PMID:1313796  
A.Accession: A42485

A.Molecule type: DNA  
A.Residues: 1-15 <MLA>  
A.Experimental source: liver  
A.Note: Sequence extracted from NCBI backbone (NCBIN:93780, NCBI:P.93787)  
R.Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagdeeswaran, P.  
Gene 41, 311-314, 1986  
A>Title: Isolation and characterization of human blood-coagulation factor X cDNA.  
A.Reference number: A25853; PMID:86221713; PMID:3011603  
A.Accession: A25853

A.Molecule type: mRNA  
A.Residues: 19-284, 'E', 289-488 <RAU>  
A.Cross-references: GB:M2613; NID:9180335; PIDN:AAA51984.1; PID:g180336  
P.Fung, M.R.; Hay, C.W.; Macgillivray, R.T.A.  
Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985  
A>Title: Characterization of an almost full-length cDNA coding for human blood coagulation  
A.Reference number: A22208; PMID:85216545; PMID:2582420  
A.Accession: A22208

A.Molecule type: mRNA  
A.Residues: 13-441, 'S', 443-488 <FUN>  
A.Cross-references: GB:K03194; NID:g182840; PIDN:AAA52490.1; PID:g182841  
R.Leytus, S.P.; Chung, D.W.; Kissel, W.; Kurachi, K.; Davie, E.W.  
Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984  
A>Title: Characterization of a cDNA coding for human factor X.  
A.Reference number: A21284; PMID:84222026; PMID:658784  
A.Accession: A21284

A.Molecule type: mRNA  
A.Residues: 13-284, 'E', 289-488 <LE2>  
A.Cross-references: GB:K01886  
R.Muchlin, B.A.; Fujikawa, K.; Kissel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weins  
Biochemistry 22, 2875-2884, 1983  
A>Title: Complete amino acid sequence of the light chain of human blood coagulation factor  
A.Reference number: A20362; PMID:83257207; PMID:6871167  
A.Accession: A20362

A.Molecule type: protein  
A.Residues: 41-179 <MCM>



F:215,291,355/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:254,300,402/Active site: His, Asp, Ser #status predicted  
Query Match 52.6%; Score 100; DB 1; Length 461;  
Best Local Similarity 45.5%; Pred. No. 3.1e-09;  
Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;  
Qy 1 ANAFLLXLRQGSILXRCCKXQCSFXXARXIFKDXARTLFWISY 44  
Db 42 ANSFLEVRAGSLRRCMEIEICDFEAEQIFQVNEIDTIAFWIKY 85  
RESULT 8  
EXCH  
coagulation factor Xa (EC 3.4.21.6) precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #text\_change 08-Dec-2000  
C:Accession: S49075; J04670; P0191; P0190; I62745  
R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.  
Thromb. Res. 80, 63-73, 1995  
A:Title: Evidence for competition between vitamin K-dependent clotting factors for intra-  
A:Accession: S49075  
A:Molecule type: mRNA  
A:Residues: 1-482 <STAL>  
A:Cross-references: EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G506601  
A:Note: submitted to the EMBL Data Library, June 1994  
A:Note: neither the complete nucleic acid sequence nor the complete translation are shown  
R:Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.  
Gene 169, 269-273, 1996  
A:Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.  
A:Reference number: J04670; MUID:96194815; PMID:8647460  
A:Accession: J04670  
A:Molecule type: protein  
A:Residues: 1-482 <STAL>  
A:Cross-references: EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G506601  
A:Experimental source: Cos-1 cell  
R:Enjuoli, K.; Miyazaki, K.; Kato, H.  
J. Biochem. 109, 890-898, 1991  
A:Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plasma  
A:Reference number: P01910; MUID:92041742; PMID:1718949  
A:Accession: P0191  
A:Molecule type: protein  
A:Residues: 41-58, 'X', 60-65 <ENJ1>  
A:Accession: P01910  
A:Molecule type: protein  
A:Residues: 181-186, 'X', 188-207 <ENJ2>  
R:Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.  
Eur. J. Haematol. 52, 162-168, 1994  
A:Title: Analysis of the partial nucleotide sequences and deduced primary structures of  
A:Reference number: I46196; MUID:94222160; PMID:8168596  
A:Accession: I46196  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 295-383 'G', 385-455 <MTR>  
A:Cross-references: GB:D1215; NID:G415309; PIDN:BA04756.1; PID:G455396  
C:Function:  
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of  
A:Pathway: blood coagulation  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-40/Domain: propeptide #status predicted <PRO>  
F:25-84/Domain: Gla domain homology <GLA>  
F:41-179/Product: coagulation factor X light chain #status predicted <LCH>  
F:90-121/Domain: EGF homology <EG1>  
F:129-164/Domain: EGF homology <EG2>  
F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>  
F:183-221/Domain: activation peptide #status predicted <APT>  
F:233-462/Product: coagulation factor Xa heavy chain #status predicted <ACT>  
F:233-460/Domain: trypsin homology <TRY>  
F:46,47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #status  
F:57-62,90-101,95-110,112-121,129-140,136-149,151-164,172-340,238-243,259-275,388-402,41

F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
F:187/Binding site: carboxylate (Asn) (covalent) #status experimental  
F:208/Binding site: carboxylate (Thr) (covalent) #status predicted  
F:218/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:231-232/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #status  
F:274,320,417/Active site: His, Asp, Ser #status predicted  
Query Match 51.6%; Score 98; DB 1; Length 482;  
Best Local Similarity 40.9%; Pred. No. 7.2e-09;  
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;  
Qy 1 ANAFLLXLRQGSILXRCCKXQCSFXXARXIFKDXARTLFWISY 44  
Db 41 ANSFEEIKKGNLERECVEERICSFEEAREVEFEDNEKTEPMNXY 84  
RESULT 9  
EXCH  
coagulation factor Xa (EC 3.4.21.6) precursor - chicken  
N:Alternate names: virus-activating proteinase  
C:Species: Gallus gallus (chicken)  
C:Date: 12-Feb-1993 #sequence revision 07-Feb-1997 #text\_change 16-Jul-1999  
C:Accession: S15838; S20380; S20381  
R:Suzuki, H.; Harada, A.; Hayaishi, Y.; Wada, K.; Asaka, J.; Gotch, B.; Ogasawara, T.; Nag  
FEBS Lett. 283, 281-285, 1991  
A:Title: Primary structure of the virus activating proteinase from chick embryo. Its identity  
A:Accession: S15838; MUID:91257322; PMID:2044767  
A:Reference number: S15838  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-475 <SZU>  
A:Cross-references: DDBJ:D00844; NID:G222869; PIDN:BA00724.1; PID:G222870  
R:Gotch, B.; Yamachi, F.; Ogasawara, T.; Nagai, Y.  
FEBS Lett. 296, 274-278, 1992  
A:Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsible  
A:Reference number: S20380; MUID:92164779; PMID:1537403  
A:Accession: S20380  
A:Molecule type: protein  
A:Residues: 41-55 <G02>  
A:Accession: S20381  
A:Molecule type: protein  
A:Residues: 241-246, 'X', 248-251, 'X', 253-261 <G0T>  
C:Function:  
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the presence of  
A:Pathway: blood coagulation  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamate  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-40/Domain: propeptide #status predicted <PRO>  
F:25-84/Domain: Gla domain homology <GLA>  
F:41-185/Product: coagulation factor X light chain #status experimental <LCH>  
F:90-121/Domain: EGF homology <EG1>  
F:129-167/Domain: EGF homology <EG2>  
F:186-475/Product: coagulation factor X heavy chain #status predicted <HCH>  
F:186-240/Domain: activation peptide #status predicted <APT>  
F:241-475/Product: coagulation factor X heavy chain #status experimental <ACT>  
F:241-468/Domain: trypsin homology <TRY>  
F:46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #status  
F:57-62,90-101,95-110,112-121,129-140,136-152,154-167,175-348,247-252,267-283,396-410,421  
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
F:106,207,228,285/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:282,328,425/Active site: His, Asp, Ser #status predicted  
Query Match 51.1%; Score 97; DB 1; Length 475;  
Best Local Similarity 40.9%; Pred. No. 1.1e-08;  
Matches 18; Conservative 9; Mismatches 17; Indels 0; Gaps 0;  
Qy 1 ANAFLLXLRQGSILXRCCKXQCSFXXARXIFKDXARTLFWISY 44  
Db 41 ANSFLEMRKQGNTERECNEERCSKEAREAREFEDNEKTEPMNXY 84  
RESULT 10



A:Molecule type: mRNA  
A:Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A',  
A:Cross-references: GB:J00136; NID:g182608; PIDN:AAA98726.1; PID:g182609  
R:Experimental source: liver  
R:Tharakan, U.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.  
Vox Sang. 58, 21-29, 1990  
A:Title: Development of an immunofluorescence assay for factor IX purification.  
A:Reference number: A60486; MUID:90194857; PMID:2316207  
A:Accession: A60486  
A:Molecule type: protein  
A:Residues: 47-52, 'XX', 55-60, 'X', 62, 'XX', 65 <THA>  
R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation factors.  
A:Reference number: A20274; MUID:83308813; PMID:6688526  
A:Accession: A20274  
A:Molecule type: protein  
A:Residues: 105-109, 'X', 111-115 <MCM>  
R:Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Sall  
Eur. J. Biochem. 172, 565-572, 1988  
A:Title: Characterization of two differently processed forms of human recombinant factor IX.  
A:Reference number: S02527; MUID:88166735; PMID:3280312  
A:Accession: S02527  
A:Molecule type: protein  
A:Residues: 29-63 <BAL>  
A:Note: processed forms expressed in recombinant system  
R:Jallat, S.; Perraud, F.; Dalemans, W.; Balland, A.; Dietzle, A.; Faure, T.; Meullen, EMO J. 9, 3255-3301, 1990  
A:Title: Characterization of recombinant human Factor IX expressed in transgenic mice and in human cells.  
A:Reference number: S12058; MUID:91006024; PMID:2209546  
A:Accession: S12058  
A:Molecule type: mRNA  
A:Residues: 1-68 <JAL>  
A:Note: processed forms expressed in recombinant system  
R:Handford, P.A.; Barton, M.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbell, EMO J. 9, 475-480, 1990  
A:Title: The first EGF-like domain from human factor IX contains a high-affinity calcium binding site.  
A:Reference number: S12377; MUID:90151623; PMID:2406129  
A:Accession: S12377  
A:Molecule type: protein  
A:Residues: 92-130 <HAN>  
A:Note: NMR detection of calcium binding by domain expressed in recombinant system  
R:de la Salle, C.; Charmanter, J.L.; Baas, M.J.; Schwartz, A.; Wiesel, M.L.; Grunbaum, Thromb. Haemost. 70, 370-371, 1993  
A:Title: A deletion located in the 3' non translated part of the factor IX gene responsible for a severe deficiency of factor IX.  
A:Reference number: I59612; MUID:9405330; PMID:8236150  
A:Accession: I59612  
A:Molecule type: DNA  
A:Status: translated from GB/EMBL/DBJ  
A:Residues: 444-461 <RES>  
A:Cross-references: GB:S66752; NID:g439773; PIDN:AA28588.1; PID:g439774  
R:Stoffel, E.S.; Koebert, D.D.; Sankar, G.; Sommer, S.S.  
Science 239, 491-494, 1988  
A:Title: Genomic amplification with transcript sequencing.  
A:Reference number: I59529; MUID:88127096; PMID:3340835  
A:Accession: I59529  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 230-359 <RE2>  
A:Cross-references: GB:M19063; NID:g182622; PIDN:AAA52456.1; PID:g182623  
R:Agarwala, K.L.; Kawabata, S.; Takao, T.; Murata, H.; Shimonishi, Y.; Nishimura, H.; Iw Biochem. Biophys. Res. Commun. 199, 5167-5171, 1994  
A:Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically linked to the protein.  
A:Reference number: A54255; MUID:94227047; PMID:8172892  
A:Accession: A54255  
A:Molecule type: protein  
A:Residues: 'P', 204, 'X', 206-211, 212, 'D', 214, 'X', 216-221, 'D', <AGA>  
A:Note: the residues designated 'x' were determined to be threonine bound to carbohydrate.  
R:Di Scipio, R.G.; Kurachi, K.; Davis, E.W.  
J. Clin. Invest. 61, 1528-1538, 1978  
A:Title: Activation of human factor IX (Christmas factor).  
A:Reference number: A18483; MUID:78194509; PMID:659613  
A:Contents: annotation; active site; carbohydrate binding

R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.  
Am. Soc. Hematol. Abstr. 64 (Suppl.1), 262a, 1984  
A:Reference number: A37569  
A:Contents: annotation  
A:Note: 194-Thr was also found  
R:Morita, T.; Isaacs, B.S.; Emon, C.T.; Johnson, A.E.  
J. Biol. Chem. 259, 5698-5704, 1984  
A:Title: Derivatives of blood coagulation factor IX contain a high affinity Ca<sup>2+</sup>-binding site.  
A:Reference number: A37543; MUID:84185715; PMID:6425256  
A:Contents: annotation; calcium binding  
R:Morita, T.; Isaacs, B.S.; Emon, C.T.; Johnson, A.E.  
J. Biol. Chem. 260, 2583, 1985  
A:Reference number: A37544  
A:Contents: annotation; calcium binding, correction  
R:Benley, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.  
Cell 45, 343-348, 1986  
A:Title: Defective propeptide processing of blood clotting factor IX caused by mutation c  
A:Reference number: A37545; MUID:86189947; PMID:3009023  
A:Contents: annotation; signal sequence cleavage site  
R:Shenoi, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya, J. Biol. Chem. 264, 21257-21265, 1989  
A:Title: Blood clotting factor IX B(M) Nagoya: substitution of arginine 180 by tryptophan  
A:Reference number: A30622; MUID:90078229; PMID:2592373  
A:Contents: annotation; sequence of mutant B(M) Nagoya  
A:Note: carboxylation, glycosylation, and cleavage sites  
R:Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownlee, submitted to the Brookhaven Protein Data Bank, November 1991  
A:Reference number: A51252; PDB:1IXA  
A:Contents: annotation; conformation by (1)H-NMR, residues 92-130  
A:Note: recombinant form expressed in yeast  
C:Comment: Factor IX is activated by factor XIa, which excises the activation peptide p  
C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K-  
C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with str  
C:Genetics:  
A:Gene: GDB:F9  
A:Cross-references: GDB:119900; OMIM:306900  
A:Map position: Xq27.1-Xq27.2  
A:Intons: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1  
A:Function:  
A:Description: catalyzes the proteolytic activation of coagulation factor X in the presen  
A:Pathway: blood coagulation intrinsic pathway  
C:Superfamily: coagulation factor X; EGF homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglut  
F:1-28/Domain: signal sequence #status experimental <SIG>  
F:29-46/Domain: propeptide #status experimental <PPT>  
F:31-91/Domain: Gla domain homology <Gla>  
F:47-191/Product: coagulation factor IXa light chain #status experimental <AUC>  
F:97-128/Domain: EGF homology <EGF>  
F:134-170/Domain: EGF homology <EG2>  
F:132-226/Domain: activation peptide #status experimental <ACT>  
F:227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>  
F:227-454/Domain: trypsin homology <TRY>  
F:53-54,61,63,66,67,72,73,76,79,82,86/Modified site: gamma-carboxyglutamic acid (Glu) #st  
F:64-69,97-108,102-117,119-128,134-145,141-155,157-170,178-235,252-268,382-396,407-435/Di  
F:99/Binding site: carbohydrate (Ser) (covalent) #status experimental  
F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
F:151-192/Cleavage site: Arg-Ala (coagulation factor IXa) #status experimental  
F:203,213/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:205,215/Binding site: carbohydrate (Thr) (covalent) #status experimental  
F:226-227/Cleavage site: Arg-Val (coagulation factor IXa) #status experimental

Query Match 46.3%; Score 88; DB 1; Length 461;  
Best Local Similarity 45.7%; Pred. No. 3; e=07;  
Matches 16; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Oy 10 QGSLRXCKXQCSFXAXRIFKAXRKLFWISY 44  
Db 57 QGDLRCHMEKCSFEBARVFNTERITRPMQY 91

RESULT 12  
KFBQ  
coagulation factor IXa (EC 3.4.21.22) precursor - bovine









Query Match 42.6%; Score 81; DB 2; Length 617;  
 Best Local Similarity 37.2%; Pred. No. 7.8e-06;  
 Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

Qy 2 NAFLXXLRQSLXRYCKXXQCSFXXRXIFKDXRTKLFWISY 44  
 :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|  
 Db 46 SGFLEELRRGNLRECVBEQCSYEAFFEALSPDPTDVFWAKY 88

Search completed: July 28, 2003, 12:25:26  
 Job time : 28 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 28, 2003, 12:12:00 ; Search time 13.5 Seconds

(without alignments)  
153.272 Million cell updates/sec

Title: SEQ3  
Perfect score: 190  
Sequence: 1 ANAFLLXRLGSLRXCKXX.....XXARXIFKXARXRLFWISY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164	86.3	466	FA7_HUMAN	P08709 Homo sapien
2	130	68.4	444	FA7_RABIT	P88139 Oryctolagus
3	119	62.6	446	FA7_MOUSE	P70375 Mus musculus
4	115	60.5	407	FA7_BOVIN	P22457 Bos taurus
5	107	56.3	492	FA10_BOVIN	P00743 Bos taurus
6	106	55.8	459	PRTC_PIG	O99182 Sus scrofa
7	105	55.3	218	TMG1_HUMAN	O14668 Homo sapien
8	104	54.7	488	FA10_HUMAN	P00742 Homo sapien
9	101	53.2	461	PRTC_MOUSE	P33587 Mus musculus
10	100	52.6	461	FA10_RABIT	P13394 Rattus norv
11	100	52.6	490	PRTC_RAT	O19045 Oryctolagus
12	97	51.1	475	FA10_CHICK	P25155 Gallus galli
13	96	50.5	456	PRTC_BOVIN	P00745 Bos taurus
14	94	49.5	231	TMG3_HUMAN	O9bzd7 Bos sapien
15	88	46.3	461	FA9_HUMAN	P00740 Bos sapien
16	87	45.8	416	FA9_BOVIN	P00741 Bos taurus
17	86	45.3	458	PRTC_RABIT	O28661 Oryctolagus
18	86	45.3	461	PRTC_HUMAN	P04070 Homo sapien
19	85	44.7	622	THRB_HUMAN	P00734 Homo sapien
20	84	44.2	376	FA10_TROCA	O14428 Tropidochelis
21	81	42.6	202	TMG2_HUMAN	O14668 Homo sapien
22	81	42.6	617	THRB_RAT	P18297 Rattus norv
23	81	42.6	618	THRB_MOUSE	P19221 Mus musculus
24	79	41.6	452	FA9_CANFA	P19540 Canis famli
25	79	41.6	459	FA9_MOUSE	P16294 Mus musculus
26	74.5	39.2	226	TMG4_HUMAN	O9bzd6 Homo sapien
27	70	36.8	649	PRTS_MACMU	O28520 Macaca mula
28	70	36.8	676	PRTS_HUMAN	P07222 Homo sapien
29	68	35.8	675	PRTS_BOVIN	P07222 Bos taurus
30	66	34.7	396	PRTZ_BOVIN	P00744 Bos taurus
31	66	34.7	646	PRTC_RABIT	P88118 Oryctolagus
32	65	34.2	625	THRB_BOVIN	P00733 Bos taurus
33	65	34.2	675	PRTS_RAT	P53813 Rattus norv

34	61	32.1	400	1	PRTZ_HUMAN	P22891 homo sapien
35	58	30.5	675	1	PRTS_MOUSE	O08761 mus musculus
36	45	23.7	879	1	YN65_YEAST	P42837 saccharomyc
37	44	23.2	2812	1	ZAN_HUMAN	O9y493 homo sapien
38	43.5	22.9	1298	1	VGR3_HUMAN	P35916 homo sapien
39	43.5	22.9	1363	1	VGR3_MOUSE	P35917 mus musculus
40	42.5	22.4	322	1	YOL3_CAEEL	O09292 caenorhabdi
41	42	22.1	263	1	PFLA_STRMU	O68575 streptococc
42	42	22.1	517	1	GUAA_VIBPA	O87807 vibrio para
43	42	22.1	1356	1	PAD3_HUMAN	O8lew0 homo sapien
44	41.5	21.8	271	1	MD12_YEAST	O92328 saccharomyc
45	41.5	21.8	1348	1	VGR2_COTUA	P52583 coturnix co

## ALIGNMENTS

RESULT 1  
ID FA7\_HUMAN STANDARD; PRT; 466 AA.  
AC P08709; O14339;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin  
DE conversion accelerator) (Epitacog alfa).  
GN F7.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=86205965; PubMed=3486420;  
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,  
RA Woodbury R.G., Hart C.E., Insley M.Y., Kissel W., Kurachi K.,  
RA Davie E.W.;  
RT "Characterization of a cDNA coding for human factor VII.";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87260948; PubMed=3037537;  
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,  
RA Hagen F.S., Murray M.J.;  
RT "Nucleotide sequence of the gene coding for human factor VII, a  
RT vitamin K-dependent protein participating in blood coagulation.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).  
RN [3]  
RP SEQUENCE FROM N.A. AND VARIANTS THR-352; GLN-413 AND LYS-445.  
RA Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,  
RA Peel C.L., Toth E.J., Yi Q., Nickerson D.A.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.  
RX MEDLINE=89088153; PubMed=3264725;  
RA Thim L., Bjørn S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,  
RA Pedersen A.H., Hedner U.;  
RT "Amino acid sequence and posttranslational modifications of human  
RT factor VIIa from plasma and transfected baby hamster kidney cells.";  
RL Biochemistry 27:7785-7793(1988).  
RN [5]  
RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.  
RX MEDLINE=91250411; PubMed=1904059;  
RA Bjørn S., Foster D.C., Thim L., Wibeberg F.C., Christensen M.,  
RA Komiyama Y., Pedersen A.H., Kissel W.;  
RT "Human plasma and recombinant factor VII. Characterization of O-  
RT glycosylations at serine residues 52 and 60 and effects of site-  
RT directed mutagenesis of serine 52 to alanine.";  
RL J. Biol. Chem. 266:11051-11057(1991).  
RN [6]  
RP STRUCTURE OF CARBOHYDRATE ON SER-112.  
RX MEDLINE=9062160; PubMed=2511201;

RA Nishimura H., Kawabata S., Kiesel W., Hase S., Ikenaka T., Takao T.,  
 RA Shimonishi Y., Iwanaga S.;  
 RA "Identification of a disaccharide (Xyl-Glc) and a trisaccharide  
 RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first  
 RT epidermal growth factor-like domain of human factors VII and IX and  
 RT protein Z and bovine protein Z.";  
 RL *J. Biol. Chem.* 264:20320-20325(1989).  
 RN [17]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-112.  
 RX MEDLINE=91344709; PubMed=2129367;  
 RA Iwanaga S., Nishimura H., Kawabata S., Kiesel W., Hase S., Ikenaka T.;  
 RT "A new trisaccharide sugar chain linked to a serine residue in the  
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";  
 RL *Adv. Exp. Med. Biol.* 281:121-131(1990).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.  
 RX MEDLINE=96175641; PubMed=8598903;  
 RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,  
 RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;  
 RT "The crystal structure of the complex of blood coagulation factor  
 RT VIIa with soluble tissue factor.";  
 RL *Nature* 380:41-46(1996).  
 RN [19]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.  
 RX MEDLINE=99126538; PubMed=923787;  
 RA Zhang B., St Charles R., Tulinsky A.;  
 RT "Structure of extracellular tissue factor complexed with factor VIIa  
 RT inhibited with a BPTI mutant.";  
 RL *J. Mol. Biol.* 285:2089-2104(1999).  
 RN [10]  
 RP STRUCTURE BY NMR OF 105-145.  
 RX MEDLINE=98367502; PubMed=9692950;  
 RA Muranyi A., Finn B.E., Gipeert G.P., Forssen S., Stenflo J.,  
 RA Driksenborg T.;  
 RT "Solution structure of the N-terminal EGF-like domain from human  
 RT factor VII.";  
 RL *Biochemistry* 37:10605-10615(1998).  
 RN [11]  
 RP VARIANT GLN-364.  
 RX MEDLINE=91300046; PubMed=2070047;  
 RA O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J.,  
 RA Meade T.W., Tuddenham E.G.D.;  
 RT "Purification and characterization of factor VII 304-Gln: a variant  
 RT molecule with reduced activity isolated from a clinically unaffected  
 RT male.";  
 RL *Blood* 78:132-140(1991).  
 RN [12]  
 RP VARIANTS GLN-364 AND PHE-370.  
 RX MEDLINE=92340074; PubMed=1634227;  
 RA Marchetti G., Patrascchini P., Gemmati D., Derosa V., Pinotti M.,  
 RA Rodozigo G., Casonato A., Girolami A., Bernardi F.;  
 RT "Detection of two missense mutations and characterization of a repeat  
 RT polymorphism in the factor VII gene (F7).";  
 RL *Hum. Genet.* 89:497-502(1992).  
 RN [13]  
 RP VARIANT TYR-238.  
 RX MEDLINE=93372811; PubMed=8364544;  
 RA Marchetti G., Ferrari M., Patrascchini P., Redaelli R., Bernardi F.;  
 RT "A missense mutation (178Gys-->Tyr) and two neutral dimorphisms  
 RT (115His and 333Ser) in the human coagulation factor VII gene.";  
 RL *Hum. Mol. Genet.* 2:1055-1056(1993).  
 RN [14]  
 RP VARIANTS.  
 RX MEDLINE=94061028; PubMed=8242057;  
 RA Takamiya O., Kembali-Cook G., Martin D.M.A., Cooper D.N.,  
 RA von Felten A., Meili E., Hahn I., Prangnelli D.R., Lumley H.,  
 RA Tuddenham E.G.D., McVey J.H.;  
 RT "Detection of missense mutations by single-strand conformational  
 RT polymorphism (SSCP) analysis in five dysfunctional variants of  
 RT coagulation factor VII.";  
 RL *Hum. Mol. Genet.* 2:1355-1359(1993).  
 RN [15]  
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.

RX MEDLINE=94264305; PubMed=8204879;  
 RA Chong S., Clarke B., Sridhara S.,  
 RA Roberts H.R., Blajchman M., Monroe D.M., High K.A.;  
 RT "Severe factor VII deficiency caused by mutations abolishing the  
 RT cleavage site for activation and altering binding to tissue factor.";  
 RL *Blood* 83:3524-3535(1994).  
 RN [16]  
 RP VARIANT VAL-354.  
 RX MEDLINE=96072589; PubMed=7981691;  
 RA Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,  
 RA Rodeghiero F., Marchetti G.;  
 RT "Topologically equivalent mutations causing dysfunctional coagulation  
 RT factors VII (294Ala-->Val) and X (334Ser-->Pro).";  
 RL *Hum. Mol. Genet.* 3:1175-1177(1994).  
 RN [17]  
 RP VARIANT MET HIS-307.  
 RX MEDLINE=95064662; PubMed=7974346;  
 RA Ohlwa M., Hayaashi T., Wada H., Minamikawa K., Shirakawa S.,  
 RA Suzuki K.;  
 RT "Factor VII Met: homozygous asymptomatic type I deficiency caused by  
 RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the  
 RT catalytic domain.";  
 RL *Thromb. Haemost.* 71:773-777(1994).  
 RN [18]  
 RP VARIANT MET-419.  
 RX MEDLINE=96247510; PubMed=8652821;  
 RA Arbini A.A., Mannucci P.M., Bauer K.A.;  
 RT "A Thr359Met mutation in factor VII of a patient with a hereditary  
 RT blood 87:5085-5094(1996).  
 RN [19]  
 RP VARIANTS TRP-283; LYS-325; VAL-358; GLN-364; GLU-402 AND GLN-413.  
 RX MEDLINE=97001216; PubMed=8844208;  
 RA Bernardi F., Castaman G., Pinotti M., Ferrarese P., di Iasio M.G.,  
 RA Lunghi B., Rodeghiero F., Marchetti G.;  
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII  
 RT deficiency.";  
 RL *Hum. Mutat.* 8:108-115(1996).  
 RN [20]  
 RP VARIANT VAL-304.  
 RX MEDLINE=97037613; PubMed=8883260;  
 RA Tamary H., Fromovich Y., Shalmon L., Retch Z., Dym O., Lanir N.,  
 RA Brenner B., Paz M., Luder A.S., Blau O., Koroletishevsky M.,  
 RA Zaitov R., Solisgoth U.;  
 RT "Ala244Val is a common, probably ancient mutation causing factor VII  
 RT deficiency in Moroccan and Iranian Jews.";  
 RL *Thromb. Haemost.* 76:283-291(1996).  
 RN [21]  
 RP VARIANT MORIOKA PRO-13.  
 RX MEDLINE=98235713; PubMed=9576180;  
 RA Ozawa T., Takikawa Y., Niya K., Ejiri N., Suzuki K., Sato S.,  
 RA Sakuragawa N.;  
 RT "Factor VII Moriooka (P11 L-26P): a homozygous missense mutation in  
 RT the signal sequence identified in a patient with factor VII  
 RT deficiency.";  
 RL *Br. J. Haematol.* 101:47-49(1998).  
 RN [22]  
 RP VARIANTS MALTA THR-194 AND VAL-304.  
 RX MEDLINE=98112461; PubMed=9452082;  
 RA Alshinawi C., Scerri C., Galdies R., Aquilina A., Felice A.E.;  
 RT "Two new missense mutations (P134T and A244V) in the coagulation  
 RT factor VII gene.";  
 RL *Hum. Mutat. Suppl.* 1:S189-S191(1998).  
 RN [23]  
 RP VARIANTS ASP-295 AND GLN-413.  
 RX MEDLINE=99318093; PubMed=10391209;  
 RA Cargill M., Althuler D., Ireland J., Sklar P., Ardile K., Patil N.,  
 RA Shaw N., Lane C.R., Lim E.P., Kalayanaraman N., Nemes J., Ziaugra L.,  
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,  
 RA Lander E.S.;  
 RT "Characterization of single-nucleotide polymorphisms in coding regions  
 RT of human genes.";  
 RL *Nat. Genet.* 22:231-238(1999).

Query Match 86.3%; Score 164; DB 1; Length 466;  
 Best Local Similarity 75.0%; Pred. No. 6,8e-22;  
 Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGSLLRKKCKXXQCSFXXARXIFPKAXRTKFWISY 44  
 61 ANAFLEELRPGSLERCKECCSEBARIFPKDAETKTLFWISY 104

RESULT 2  
 ID\_FAT7 RABIT STANDARD; PRT; 444 AA.  
 AC P98139; P79224;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Coagulation factor VII precursor (BC 3.4.21.21) (Serum prothrombin conversion accelerator).  
 GN F7.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=93190306; PubMed=8383365;  
 RA Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;  
 RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII."  
 RL Thromb. Res. Suppl. 69:231-238 (1993).  
 RN [2]  
 RP REVISION TO 395.  
 RC TISSUE=Liver;  
 RA Ritz S.R., Blajchman M.A., Clarke B.J.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS CONVERTED TO FACTOR VIIA BY FACTOR XIIA, FACTOR IXA, OR THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to form factor Xa.  
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED BY A DISULFIDE BOND (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: Plasma.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: Contains 2 EGF-like domains.  
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 CC  
 DR EMBL; U74777; AAB37326.1; -  
 DR HSP; P08709; 1FAK.  
 DR MEROPS; S01.215; -  
 DR InterPro; IPR000152; Aex\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001438; EGF\_11.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR002383; GLA\_blood.

DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF\_2.  
 DR Pfam; PF00594; gla\_1.  
 DR Pfam; PF00089; trypsin\_1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00010; EGFBLD.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA\_1.  
 DR SMART; SM00069; GLA\_1.  
 DR SMART; SM00020; TRYD\_SPC\_1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL\_1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS0106; EGF\_2; 1.  
 DR PROSITE; PS0107; EGF\_CA\_1.  
 DR PROSITE; PS00011; GLU\_CARBOXYLATION\_1.  
 DR PROSITE; PS00240; TRYPSIN\_DOM\_1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER\_1.  
 KW Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein; Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid; EGF-like domain; Repeat; Signal; Hydroxylation.  
 KW EGF-like domain; Repeat; Signal; Hydroxylation.  
 FT SIGNAL 1 21  
 FT PROPEP 22 39  
 FT CHAIN 40 191  
 FT CHAIN 192 444  
 FT DOMAIN 45 74  
 FT DOMAIN 85 121  
 FT DOMAIN 126 167  
 FT DOMAIN 192 444  
 FT SITE 191 192  
 FT ACT\_SITE 232 232  
 FT ACT\_SITE 281 281  
 FT ACT\_SITE 383 383  
 FT BINDING 377 377  
 FT DISULFID 56 61  
 FT DISULFID 89 100  
 FT DISULFID 94 109  
 FT DISULFID 111 120  
 FT DISULFID 130 141  
 FT DISULFID 137 151  
 FT DISULFID 153 166  
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 FT MOD\_RES 65 65  
 FT MOD\_RES 68 68  
 FT MOD\_RES 74 74  
 FT MOD\_RES 102 102  
 FT MOD\_RES 211 211  
 FT CARBOHYD 242 242  
 FT CARBOHYD 306 306  
 SO SEQUENCE 444 AA; 49011 MW; 0481ABCAFE5427F8 CRC64;

Query Match 68.4%; Score 130; DB 1; Length 444;  
 Best Local Similarity 56.8%; Pred. No. 9,4e-16;  
 Matches 25; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGSLLRKKCKXXQCSFXXARXIFPKAXRTKFWISY 44  
 40 ANAFLEELRPGSLERCKECCSEBARIFPKDAETKTLFWISY 83

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RESULT 3
FA7_MOUSE STANDARD; PRT; 446 AA.
AC P70375;
DT 01-NOV-1997 (Rel. 35, Last Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
DE F7 OR CF7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97127167; PubMed=8972017;
RA Idusoglyc E., Rosen E.D., Carmeliet P., Collen D., Castellino F.J.;
RT "Nucleotide structure and characterization of the murine blood
RT coagulation factor VII gene."
RL Thromb. Haemost. 76:957-964 (1996).
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa OR
CC AND CALCIUM IONS. FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- PMW: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib.ch).
CC -----
CC EMBL; U66079; AAC3796.1; -.
DR HSSP; P08709; 1BF9.
DR MEROPS; S01.215; -.
DR MGD; MGI:109325; F7.
DR InterPro; IPR000152; Asx hydroyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF-II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBLD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS01187; EGF_CA; 1.
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DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat; Signal; Hydroxylation.
FT SIGNAL 1 24
FT PROPEP 25 41
FT CHAIN 42 193
FT CHAIN 194 446
FT DOMAIN 47 76
FT DOMAIN 87 123
FT DOMAIN 128 169
FT DOMAIN 194 446
FT SITE 193 194
FT ACT_SITE 234 234
FT ACT_SITE 283 283
FT ACT_SITE 385 385
FT BINDING 379 379
FT DISULFID 58 63
FT DISULFID 91 102
FT DISULFID 96 111
FT DISULFID 113 122
FT DISULFID 132 143
FT DISULFID 139 153
FT DISULFID 155 168
FT DISULFID 176 303
FT DISULFID 200 205
FT DISULFID 219 235
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FT DISULFID 381 409
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FT MOD_RES 55 55
FT MOD_RES 57 57
FT MOD_RES 60 60
FT MOD_RES 61 61
FT MOD_RES 66 66
FT MOD_RES 67 67
FT MOD_RES 70 70
FT MOD_RES 76 76
FT MOD_RES 104 104
FT MOD_RES 186 186
FT CARBOHYD 244 244
SQ SEQUENCE 446 AA; 50276 MW; 2512844A45CE96E CRC64;

Query Match 62.6%; Score 119; DB 1; Length 446;
Best Local Similarity 56.8%; Pred. No. 9.3e-14;
Matches 25; Conservative 1; Mismatches 18; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRGSLRXCKXQCSFXRXKXFKKXKRLKFWISY 44
Db 42 ANSLLEIWPGLSEKNEECSEFEAREIIFKSPERTKQFWIVY 85

RESULT 4
FA7_BOVIN STANDARD; PRT; 407 AA.
AC P22457;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion
DE accelerator).
DE F7.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
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RP SEQUENCE.  
 RX MEDLINE=69008362; PubMed=1049594;  
 RA Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,  
 RT Iwanaga S.,  
 RT "Bovine factor VII. Its purification and complete amino acid  
 sequence.";  
 RL J. Biol. Chem. 263:14868-14877(1988).  
 RN [2]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-52.  
 RX MEDLINE=9213999; PubMed=3149637;  
 RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,  
 RA Miyata T., Iwanaga S., Takao T., Shimonishi Y., Ikenaka T.;  
 RT "A new trisaccharide sugar chain linked to a serine residue in bovine  
 RT blood coagulation factors VII and IX.";  
 RL J. Biochem. 104:867-868(1988).  
 RN [3]  
 RP STRUCTURE OF CARBOHYDRATE ON SER-52.  
 RX MEDLINE=91344709; PubMed=2129367;  
 RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;  
 RT "A new trisaccharide sugar chain linked to a serine residue in the  
 RT first EGF-like domain of clotting factors VII and IX and protein Z.";  
 RL Adv. Exp. Med. Biol. 281:121-131(1990).  
 CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS  
 CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR  
 CC THROMBIN BY MINOR PROTEOLYSES. IN THE PRESENCE OF TISSUE FACTOR  
 CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa  
 CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO  
 CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.  
 CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to  
 CC form factor Xa.  
 CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED  
 CC BY A DISULFIDE BOND.  
 CC -1- TISSUE SPECIFICITY: Plasma.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: Contains 2 EGF-like domains.  
 CC PIR: A31979; KPE07.  
 DR HSSP: P08709; 1BP9.  
 DR MEROPS: S01.215; -;  
 DR InterPro: IPR000152; Asx\_hydroxy1.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR000742; EGF 2.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR001438; EGF\_II.  
 DR InterPro: IPR006209; EGF\_III.  
 DR InterPro: IPR002383; GLA blood.  
 DR InterPro: IPR001254; Ser protease\_Try.  
 DR InterPro: IPR000294; VitK\_dep\_GLA.  
 DR Pfam: PF00008; EGF; 2.  
 DR Pfam: PF00594; Gla; 1.  
 DR Pfam: PF00089; trypsin; 1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR PRINTS: PR00010; EGFBL00D.  
 DR PRINTS: PR00001; GLABLOD.  
 DR SMART: SM00179; EGF\_Ca; 1.  
 DR SMART: SM00069; GLA; 1.  
 DR SMART: SM00020; TRYF\_SPC; 1.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE: PS00022; EGF\_1; 1.  
 DR PROSITE: PS01186; EGF\_2; 2.  
 DR PROSITE: PS01187; EGF\_Ca; 1.  
 DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE: PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 KM Hydrolyase: Serine protease; Blood coagulation; Zymogen; Glycoprotein;  
 KM Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;  
 KM EGF-like domain; Repeat.  
 FT CHAIN 1 152 FACTOR VII LIGHT CHAIN.  
 FT CHAIN 153 407 FACTOR VII HEAVY CHAIN.  
 FT DOMAIN 6 35 GLA-RICH.

FT DOMAIN 46 82 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 87 128 EGF-LIKE 2.  
 FT DOMAIN 153 407 SERINE PROTEASE.  
 FT SITE 152 153 CLEAVAGE (BY FACTOR Xa, FACTOR XIa,  
 FT FACTOR IXa, OR THROMBIN).  
 FT ACT\_SITE 193 193 BY SIMILARITY.  
 FT ACT\_SITE 242 242 BY SIMILARITY.  
 FT ACT\_SITE 344 344 BY SIMILARITY.  
 FT BINDING 338 338 SUBSTRATE (BY SIMILARITY).  
 FT DISULFID 17 22 BY SIMILARITY.  
 FT DISULFID 50 61 BY SIMILARITY.  
 FT DISULFID 55 70 BY SIMILARITY.  
 FT DISULFID 72 81 BY SIMILARITY.  
 FT DISULFID 91 102 BY SIMILARITY.  
 FT DISULFID 98 112 BY SIMILARITY.  
 FT DISULFID 114 127 BY SIMILARITY.  
 FT DISULFID 135 262 BY SIMILARITY.  
 FT DISULFID 159 164 BY SIMILARITY.  
 FT DISULFID 178 194 BY SIMILARITY.  
 FT DISULFID 310 329 BY SIMILARITY.  
 FT DISULFID 340 368 BY SIMILARITY.  
 FT MOD\_RES 6 6 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 16 16 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 19 19 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 25 25 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 29 29 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 35 35 GAMMA-CARBOXYGLUTAMIC ACID.  
 FT MOD\_RES 52 52 O-LINKED (GLC..).  
 FT CARBOHYD 145 145 N-LINKED (GLCNAC..).  
 FT CARBOHYD 203 203 N-LINKED (GLCNAC..).  
 SQ SEQUENCE 407 AA; 44431 MW; 703E1FE0636F7F10 CRC64;

Query Match 60.5%; Score 115; DB 1; Length 407;  
 Best Local Similarity 50.0%; Pred. No. 4, 5e-13;  
 Matches 22; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANAFLLXRLQGSLLKRYCKXQCSFXXARKIFKDXARTKLFWISY 44  
 1 ANGFLLEELPLGSLERECREBELCSFEENHEIFRBERETRPQWVSAY 44

RESULT 5  
 ID PA10 BOVIN STANDARD; PRT; 492 AA.  
 AC P00743;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).  
 GN F10.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE OF 1-487 FROM N.A.  
 RX MEDLINE=84247315; PubMed=6330671;  
 RA Fung M.R., Campbell R.W., McGillivray R.T.A.;  
 RT "Blood coagulation factor X mRNA encodes a single polypeptide chain  
 RT containing a prepro leader sequence.";  
 RL Nucleic Acids Res. 12:4481-4492(1984).  
 RN [2]  
 RP SEQUENCE OF 41-180  
 RX MEDLINE=60130563; PubMed=6766735;  
 RA Eitfeld D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,  
 RA Titani K.;  
 RT "Amino acid sequence of the light chain of bovine factor XI (Stuart  
 RT factor).";

RL Biochemistry 19:659-667(1980).  
 RN [3]  
 RA REVISION TO 103.  
 RX MEDLINE=83308813; PubMed=6668526;  
 RA McMullen B.A., Fujikawa K., Kiesel M.;  
 RT "The occurrence of beta-hydroxyaspartic acid in the vitamin  
 RT K-dependent blood coagulation zymogens."  
 RL Biochem. Biophys. Res. Commun. 115:8-14(1983).  
 RN [4]  
 RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.  
 RX MEDLINE=76053069; PubMed=1059093;  
 RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,  
 RA Neurath H.;  
 RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy  
 RT chain."  
 RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).  
 RN [5]  
 RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=94062825; PubMed=8243461;  
 RA Inoue K., Morita T.;  
 RT "Identification of O-linked oligosaccharide chains in the activation  
 RT peptides of blood coagulation factor X. The role of the carbohydrate  
 RT moieties in the activation of factor X."  
 RL Eur. J. Biochem. 218:153-163(1993).  
 RN [6]  
 RP ACTIVE SITE.  
 RX MEDLINE=73053114; PubMed=4264286;  
 RA Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,  
 RA Neurath H., Davie E.W.;  
 RT "Bovine factor X Ia (activated Stuart factor). Evidence of homology  
 RT with mammalian serine proteases."  
 RL Biochemistry 11:4899-4903(1972).  
 RN [7]  
 RP PROCESSING.  
 RX MEDLINE=76053121; PubMed=1059122;  
 RA Fujikawa K., Titani K., Davie E.W.;  
 RT "Activation of bovine factor X (Stuart factor): conversion of factor  
 RT Xa-alpha to factor Xa-beta."  
 RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).  
 RN [8]  
 RP CALCIUM-BINDING DATA.  
 RX MEDLINE=84185716; PubMed=6546930;  
 RA Sugo T., Bjoerk I., Holmgren A., Stenflo J.;  
 RT "Calcium-binding properties of bovine factor X lacking the gamma-  
 RT carboxyglutamic acid-containing region."  
 RL J. Biol. Chem. 259:5705-5710(1984).  
 RN [9]  
 RP SUPFATION  
 RX MEDLINE=86140210; PubMed=3949800;  
 RA Morita T., Jackson C.M.;  
 RT "Localization of the structural difference between bovine blood  
 RT coagulation factors XI and X2 to tyrosine 18 in the activation  
 RT peptide."  
 RL J. Biol. Chem. 261:4008-4014(1986).  
 RN [10]  
 RP STRUCTURE BY NMR OF 85-126.  
 RX MEDLINE=91084483; PubMed=2261466;  
 RA Selander M., Persson E., Stenflo J., Drakenberg T.;  
 RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of  
 RT the amino-terminal epidermal growth factor like domain in coagulation  
 RT factor X."  
 RL Biochemistry 29:8111-8118(1990).  
 RN [11]  
 RP STRUCTURE BY NMR OF 85-126.  
 RX MEDLINE=92329412; PubMed=1627540;  
 RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,  
 RA Telemann O.;  
 RT "Three-dimensional structure of the apo form of the N-terminal  
 RT EGF-like module of blood coagulation factor X as determined by NMR  
 RT spectroscopy and simulated folding."  
 RL Biochemistry 31:5974-5983(1992).  
 RN [12]  
 RP STRUCTURE BY NMR OF 85-126.

RX MEDLINE=92406922; PubMed=1527084;  
 RA Selander-Sunnerhagen M., Ullner M., Persson E., Telemann O.,  
 RA Stenflo J., Drakenberg T.;  
 RT "How an epidermal growth factor (EGF)-like domain binds calcium. High  
 RT resolution NMR structure of the calcium form of the NH2-terminal EGF-  
 RT like domain in coagulation factor X."  
 RL J. Biol. Chem. 267:19642-19649(1992).  
 RN [13]  
 RP STRUCTURE BY NMR OF 41-126.  
 RX MEDLINE=96387194; PubMed=8794734;  
 RA Sunnerhagen M., Olan G.A., Stenflo J., Foren S., Drakenberg T.,  
 RA Trewhella J.;  
 RT "The relative orientation of Gla and EGF domains in coagulation  
 RT factor X is altered by Ca2+ binding to the first EGF domain. A  
 RT combined NMR-small angle X-ray scattering study."  
 RL Biochemistry 35:11547-11559(1996).  
 CC -I- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 CC converts prothrombin to thrombin in the presence of factor Va,  
 CC calcium and phospholipid during blood clotting.  
 CC -I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 CC Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -I- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 CC MORE DISULFIDE BONDS.  
 CC -I- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -I- PTM: N- AND O-GLYCOSYLATED.  
 CC -I- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 CC INTRINSIC PATHWAY) OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).  
 CC -I- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.  
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -I- SIMILARITY: Contains 2 EGF-like domains.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X00673; CAA25286.1; -.  
 DR PIR; A22867; EXBO.  
 DR PDB; 1APO; 31-JAN-94.  
 DR PDB; 1CCF; 31-MAY-94.  
 DR PDB; 1WHE; 15-MAY-97.  
 DR PDB; 1WHF; 15-MAY-97.  
 DR PDB; 1IOD; 21-JAN-03.  
 DR PDB; 1KIG; 28-OCT-98.  
 DR MEROPS; S01.216; -.  
 DR GlycoSuiteDB; P00743; -.  
 DR InterPro; IPR000152; Aa\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000742; EGF 2.  
 DR InterPro; IPR001881; EGF Ca.  
 DR InterPro; IPR006209; EGF\_Like.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VltK\_dep\_GLA.  
 DR Pfam; PF00008; EGF\_2.  
 DR Pfam; PF00594; Gla; 1.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 1.



Query Match	56.3%	Score 107;	DB 1;	Length 492;
Best Local Similarity	45.5%	Pred. No. 1.6e-11;		
Matches 20; Conservative	7;	Mismatches 17;	Indels 0;	Gaps 0;

RESULT 6	
PRTC_PIG	
ID_PRTC_PIG	STANDARD;
	PRT; 459 AA

CC		strongly promoted by thrombomodulin.
CC	-1-	TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC	-1-	PM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.
CC	-1-	MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the Gla domain. This Gla-independent binding site is necessary for the recognition of the thrombin-thrombomodulin complex.
CC	-1-	SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC	-1-	SIMILARITY: Contains 2 EGF-like domains.
CC		-----
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch">http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch</a> ).
CC		-----
DR	EMBL;	AF191307; AAG28380.1; -.
DR	HSSP;	P04070; IPCU.
DR	MEROPS;	S01_218; -.
DR	InterPro;	IPR000152; Asx_hydroxyl.
DR	InterPro;	IPR001314; Chymotrypsin.
DR	InterPro;	IPR001881; EGF_Ca.
DR	InterPro;	IPR006209; EGF_Like.
DR	InterPro;	IPR002383; Gla_blood.
DR	InterPro;	IPR006210; IEgf.
DR	InterPro;	IPR001254; Ser_protease_Try.
DR	InterPro;	IPR000294; VitK_dep_Gla.
DR	Pfam;	PF00008; EGF_2.
DR	Pfam;	PF00594; Glf_1.
DR	Pfam;	PF00089; trypsin_1.
DR	PRINTS;	PR00722; CHYMOTRYPSIN.
DR	PRINTS;	PR00001; GLABLOOD.
DR	SMART;	SM00181; EGF_2.
DR	SMART;	SM00069; Gla_1.
DR	SMART;	SMO0020; TRYP_Spc; 1.
DR	PROSITE;	PS00010; ASX_HYDROXYL_1.
DR	PROSITE;	PS00022; EGF_1; 1.
DR	PROSITE;	PS00186; EGF_2; 2.
DR	PROSITE;	PS01187; EGF_CA_1.
DR	PROSITE;	PS00011; GLU_CARBOXYLATION; 1.
DR	PROSITE;	PS50240; TRYPSIN_DOM; 1.
DR	PROSITE;	PS00134; TRYPSIN_HIS; 1.
DR	PROSITE;	PS00135; TRYPSIN_SER; 1.
KW	Blood coagulation;	Glycoprotein; Serine protease;
KW	Gamma-carboxyglutamic acid;	Calcium-binding; Vitamin K; Hydroxylation;
KW	EGF-like domain;	Repeat; Endothelial cell; Hydrolase; Signal.
FT	SIGNAL	1 18 BY SIMILARITY.
FT	PROPEP	19 41 EGF-LIKE 2.
FT	CHAIN	42 459 SERINE PROTEASE.
FT	CHAIN	42 459 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	CHAIN	42 196 SIMILARITY).
FT	CHAIN	199 459 PROTEIN C HEAVY CHAIN (BY
FT	CHAIN	199 459 SIMILARITY).
FT	PEPTIDE	199 213 ACTIVATION PEPTIDE (BY SIMILARITY).
FT	SITE	213 214 CLEAVAGE (BY THROMBIN) (BY
FT	SITE	213 214 SIMILARITY).
FT	DOMAIN	96 131 EGF-LIKE 1.
FT	DOMAIN	135 175 EGF-LIKE 2.
FT	DOMAIN	214 459 SERINE PROTEASE.
FT	MOD_RES	47 47 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	48 48 SIMILARITY).
FT	MOD_RES	48 48 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	55 55 SIMILARITY).
FT	MOD_RES	55 55 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	57 57 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	57 57 SIMILARITY).
FT	MOD_RES	60 60 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	60 60 SIMILARITY).
FT	MOD_RES	61 61 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT	MOD_RES	61 61 SIMILARITY).

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FT MOD_RES 66 66 SIMILARITY).
FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID (BY
FT MOD_RES 112 112 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 255 255 CHARGE RELAY SYSTEM.
FT ACT_SITE 301 301 CHARGE RELAY SYSTEM.
FT ACT_SITE 400 400 CHARGE RELAY SYSTEM.
FT DISULFID 58 63 BY SIMILARITY.
FT DISULFID 91 110 BY SIMILARITY.
FT DISULFID 100 105 BY SIMILARITY.
FT DISULFID 104 119 BY SIMILARITY.
FT DISULFID 121 130 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 146 159 BY SIMILARITY.
FT DISULFID 161 174 BY SIMILARITY.
FT DISULFID 182 321 INTERCHAIN (BY SIMILARITY).
FT DISULFID 240 256 BY SIMILARITY.
FT DISULFID 371 385 BY SIMILARITY.
FT DISULFID 396 424 BY SIMILARITY.
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;
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Query Match 55.8%; Score 106; DB 1; Length 459;
Best Local Similarity 47.7%; Pred. No. 2.2e-11;
Matches 21; Conservative 3; Mismatches 20; Indels 0; Gaps 0;
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OY 1 ANAFLXLRQGSILRXCKXQCSFXXARXIFKDXARTKLFWISY 44
DB 42 ANSFLEELRPSLSRECKEETCDFEAREEIFONTENTWAFMSKY 85
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RESULT 7
TMG1_HUMAN STANDARD; PRT; 218 AA.
ID TMG1_HUMAN STANDARD; PRT; 218 AA.
AC 014668;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Proline-
rich Gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein
1).
GN PRG1 OR TMG1 OR PRG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97404347; PubMed=9256434;
RA Kulman J.B., Harris J.E., Haldeman B.A., Davie E.W.;
RT "Primary structure and tissue distribution of two novel proline-rich
gamma-carboxyglutamic acid proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
CC -1- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
CC -1- PTH: Gla residues are produced after subsequent posttranslational
modifications of glutamic acid by a vitamin K-dependent gamma-
carboxylase.
CC -----
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CC -----
CC EMBL; AF009242; AAB67070.1; -.
```

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DR HSPB; P00740; 1CFH.
DR Genew; HGNC:9469; PRG1.
DR MIM; 604428; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR00294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; vitamin K; Transmembrane.
FT PROPEP 1 20 POTENTIAL.
FT CHAIN 1 218 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT DOMAIN 21 83 PROTEIN 1.
FT TRANSMEM 84 106 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 107 218 POTENTIAL.
FT DOMAIN 124 61 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 131 135 GLA-RICH.
SQ SEQUENCE 218 AA; 24947 MW; 26538A61AB0AEB98 CRC64;
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Query Match 55.3%; Score 105; DB 1; Length 218;
Best Local Similarity 43.2%; Pred. No. 1.5e-11;
Matches 19; Conservative 8; Mismatches 17; Indels 0; Gaps 0;
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OY 1 ANAFLXLRQGSILRXCKXQCSFXXARXIFKDXARTKLFWISY 44
DB 21 ANGFEEIRQGNIERECKEETCFEAREAREENNEKTKFEWISY 64
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## RESULT 8

```
FA10_HUMAN STANDARD; PRT; 488 AA.
ID FA10_HUMAN STANDARD; PRT; 488 AA.
AC P00742; O14340;
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DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91216473; PubMed=1902434;
RA Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
human coagulation factor X.";
RL Gene 99:291-294(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87026600; PubMed=3768336;
RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
RT "Gene for human factor X: a blood coagulation factor whose gene
organization is essentially identical with that of factor IX and
protein C.";
RL Biochemistry 25:5098-5102(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Ozuna M., Peol C.L., Toch E.J., Yi O., Nickerson D.A.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 13-488 FROM N.A.
RX MEDLINE=85216545; PubMed=2582420;
RA Fung M.R., Hay C.W., McGillivray R.T.A.;
RT "Characterization of an almost full-length cDNA coding for human
blood coagulation factor X.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
RN [5]
RP SEQUENCE OF 19-488 FROM N.A.
RC TISSUE=Liver;
```

RX MEDLINE=6621713; PubMed=3011603;  
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;  
 RT "Isolation and characterization of human blood-coagulation factor X  
 cDNA";  
 RL Gene 41:311-314(1986).  
 RN [6]  
 RP SEQUENCE OF 41-179.  
 RX MEDLINE=9325207; PubMed=6871167;  
 RA McMullen B.A., Fujikawa K., Kistiel W., Sasagawa T., Howald W.N.,  
 RA Kwa E.Y., Weinstein B.;  
 RT "Complete amino acid sequence of the light chain of human blood  
 coagulation factor X: evidence for identification of residue 63 as  
 beta-hydroxyaspartic acid.";  
 RL Biochemistry 22:2875-2884(1983).  
 RN [7]  
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.  
 RC TISSUE=LIVER;  
 RX MEDLINE=84222026; PubMed=5587384;  
 RA Leytue S.P., Chung D.W., Kistiel W., Kurachi K., Davie E.W.;  
 RT "Characterization of a cDNA coding for human factor X.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).  
 RN [8]  
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=94062825; PubMed=8243461;  
 RA Inoue K., Morita T.;  
 RT "Identification of O-linked oligosaccharide chains in the activation  
 peptides of blood coagulation factor X. The role of the carbohydrate  
 moieties in the activation of factor X.";  
 RL Eur. J. Biochem. 218:153-163(1993).  
 RN [9]  
 RP SEQUENCE OF 1-23 FROM N.A.  
 RX MEDLINE=90128299; PubMed=2612918;  
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhanam K., Lyman G.;  
 RT "Cloning and characterization of the 5' end (exon 1) of the gene  
 encoding human factor X.";  
 RL Gene 84:517-519(1989).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=93360277; PubMed=8355279;  
 RA Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode W.,  
 RA Huber R., Blankenship D.T., Cardin A.D., Kistiel W.;  
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";  
 RL J. Mol. Biol. 232:947-966(1993).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=98283982; PubMed=9618463;  
 RA Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;  
 RT "Structural basis for chemical inhibition of human blood coagulation  
 factor Xa.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).  
 RN [12]  
 RP VARIANTS ILE-7 AND HIS-30.  
 RX MEDLINE=99318093; PubMed=10391209;  
 RA Cargill M., Althuler D., Ireland J., Sklar P., Ardlie K., Patil N.,  
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,  
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,  
 RA Lander E.S.;  
 RT "Characterization of single-nucleotide polymorphisms in coding regions  
 of human genes";  
 RL Nat. Genet. 22:231-238(1999).  
 RN [13]  
 RP ERRATUM.  
 RA Cargill M., Althuler D., Ireland J., Sklar P., Ardlie K., Patil N.,  
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,  
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,  
 RA Lander E.S.;  
 RT "Genet. 23:373-373(1999)."  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 converts prothrombin to thrombin in the presence of factor Va,  
 calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR

CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 CC MORE DISULFIDE BONDS.  
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -1- PTM: N- AND O-GLYCOSYLATED.  
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: Contains 2 EGF-like domains.  
 CC -----  
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; K03194; AA52490.1; -;  
 DR EMBL; M57285; AA52421.1; -;  
 DR EMBL; AF503510; AA019347.1; -;  
 DR EMBL; L29433; AA52764.1; -;  
 DR EMBL; L00390; AA52764.1; JOINED.  
 DR EMBL; L00391; AA52764.1; JOINED.  
 DR EMBL; L00392; AA52764.1; JOINED.  
 DR EMBL; L00393; AA52764.1; JOINED.  
 DR EMBL; L00394; AA52764.1; JOINED.  
 DR EMBL; L00395; AA52764.1; JOINED.  
 DR EMBL; L00396; AA52764.1; JOINED.  
 DR EMBL; M22613; AA51984.1; -;  
 DR EMBL; K01886; AA52486.1; -;  
 DR EMBL; M33297; AA52636.1; -;  
 DR PIR; A24478; EXRU.  
 DR PDB; 1HCQ; 08-MAY-95.  
 DR PDB; 1FAX; 29-OCT-97.  
 DR PDB; 1FXY; 17-JUN-98.  
 DR PDB; 1XKA; 23-MAR-99.  
 DR PDB; 1XKB; 23-MAR-99.  
 DR PDB; 1EZQ; 20-SEP-00.  
 DR PDB; 1FOR; 20-SEP-00.  
 DR PDB; 1FOS; 20-SEP-00.  
 DR PDB; 1FJS; 17-NOV-00.  
 DR PDB; 1G2L; 20-OCT-01.  
 DR PDB; 1G2M; 20-OCT-01.  
 DR PDB; 1KSN; 19-JUN-02.  
 DR PDB; 1KYE; 11-FEB-03.  
 DR PDB; 1MO5; 28-JAN-03.  
 DR PDB; 1MO6; 28-JAN-03.  
 DR PDB; 1NEU; 25-FEB-03.  
 DR PDB; 1NEW; 25-FEB-03.  
 DR PDB; 1NFX; 25-FEB-03.  
 DR PDB; 1NFY; 25-FEB-03.  
 DR MEROPS; S01.216; -;  
 DR GlycoSiteDB; P00742; -;  
 DR Genew; HGNC:3528; F10.  
 DR MIM; 134530; -;  
 DR MIM; 227600; -;  
 DR GO; GO:0005576; C:extracellular; TAS.  
 DR GO; GO:0003804; F:Blood coagulation factor X activity; TAS.  
 DR GO; GO:0007596; P:Blood coagulation; TAS.  
 DR InterPro; IPR000152; Axx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001438; EGF\_II.  
 DR InterPro; IPR006209; EGF\_II.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00594; gla; 1.

```

DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBLD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRYP_SPE; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.

Query Match          54.7% Score 104; DB 1; Length 488;
Best Local Similarity 40.9% Pred. No. 5,4e-11;
Matches 18; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRQSLKRXCKXQCFYKXRXIFKDXARTLFWISY 44
Db 41 ANSFLEEMKKGHLRECHMETCSYEAREVEFEDSDKTNEFWNKY 84

RESULT 9
PRTC_MOUSE
ID PRTC_MOUSE STANDARD; PRT; 461 AA.
AC P33587; O35498;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92316897; PubMed=1618739;
RA Tada N., Sato M., Teujimura A., Iwase R., Hashimoto-Gotoh T.;
RT "Isolation and characterization of a mouse protein C cDNA.";
RL J. Biochem. 111:491-495(1992).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX MEDLINE=96152576; PubMed=9493582;
RA Jallbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,
RT "Nucleotide structure and characterization of the murine gene encoding anticoagulant protein C.";
RL Thromb. Haemost. 79:310-316(1998).
RN (3)
RP SEQUENCE OF 274-434 FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=94318474; PubMed=8043441;
RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Nihio Y.;
RT "A comparative study of partial primary structures of the catalytic region of mammalian protein C.";
RL Br. J. Haematol. 86:590-600(1994).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIIa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN. THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLY PROMOTED BY THROMBOMODULIN.

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CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING SITE IS NECESSARY FOR THE RECOGNITION OF THE THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
-----
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CC EMBL; D10445; BAA01235.1; -.
CC EMBL; AF034569; AAC33795.1; -.
CC EMBL; D43755; BAA07812.1; -.
CC PIR; JX0210; JX0210.
CC HSSP; P04070; 1PCU.
CC MEROPS; S01.218; -.
CC MGD; MGI:97771; Proc.
CC InterPro; IPR000152; Asx hydroxyl.
CC InterPro; IPR001314; Chymotrypsin.
CC InterPro; IPR001881; EGF Ca.
CC InterPro; IPR006209; EGF_Like.
CC InterPro; IPR002383; GLA_Blood.
CC InterPro; IPR001254; Ser protease TRY.
CC InterPro; IPR000294; VitK_dep_GLA.
CC Pfam; PF00008; EGF; 2.
CC Pfam; PF00594; Glu; 1.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00001; GLABLOOD.
CC SMART; SM00179; EGF_CA; 1.
CC SMART; SM00069; GLA; 1.
CC SMART; SM00020; TRYP_SPE; 1.
CC PROSITE; PS00010; ASX_HYDROXYL; 1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; 2.
CC PROSITE; PS01187; EGF_CA; 1.
CC PROSITE; PS00011; GLU_CARBOXYLATION; 1.
CC PROSITE; PS50240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
FT SIGNAL 1 33
FT PROPEP 34 41
FT CHAIN 42 196
FT CHAIN 199 461
FT PEPTIDE 199 212
FT SITE 212 213
FT DONAIN 96 131
FT DONAIN 135 175
FT DONAIN 213 461
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
FT MOD_RES 57 57
FT MOD_RES 60 60
FT MOD_RES 61 61
FT MOD_RES 66 66

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FT	MOD_RES	67	67	(BY SIMILARITY). GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	70	70	(BY SIMILARITY). GAMMA-CARBOXYGLUTAMIC ACID (BY SIMILARITY).
FT	MOD_RES	112	112	HYDROXYLATION (BY SIMILARITY).
FT	ACT_SITE	253	253	CHARGE RELAY SYSTEM.
FT	ACT_SITE	289	299	CHARGE RELAY SYSTEM.
FT	ACT_SITE	402	402	CHARGE RELAY SYSTEM.
FT	DISULFID	58	63	BY SIMILARITY.
FT	DISULFID	91	110	BY SIMILARITY.
FT	DISULFID	100	105	BY SIMILARITY.
FT	DISULFID	104	119	BY SIMILARITY.
FT	DISULFID	121	130	BY SIMILARITY.
FT	DISULFID	139	150	BY SIMILARITY.
FT	DISULFID	146	159	BY SIMILARITY.
FT	DISULFID	161	174	BY SIMILARITY.
FT	DISULFID	182	319	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	238	254	BY SIMILARITY.
FT	DISULFID	373	387	BY SIMILARITY.
FT	DISULFID	398	426	BY SIMILARITY.
FT	CARBOHYD	214	214	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	290	290	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	355	355	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	328	328	MISSING (IN REF. 2).
FT	CONFLICT	393	393	N -> D (IN REF. 2).
SO	SEQUENCE	461 AA;	51945 MW;	53FNAOD85B194D6E CRC64;

Query Match	53.2%	Score 101	DB 1	Length 461
Best Local Similarity	45.5%	Pred. No. 1.8e-10		
Matches 20	Conservative 5	Mismatches 19	Indels 0	Gaps 0

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QY      1 ANAFLXLRQGSLRXKCKKKQCSFXXARXIFKDAXRTYLFWISY 44
        ||| : |||| | : ||: |||
Db     42 ANSFLEMRPGSLERECMEICDFEEAQEIFQNVEDTLAFWIKY 85
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RESULT 10	
PRTC_RAT	
ID_PRTC_RAT	STANDARD;
	PRT; 461 AA

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Vitamin-K-dependent protein C precursor (BC 3.4.21.69)

DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).

GN PROC.

OS *Rattus norvegicus* (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

[1]

RN SEQUENCE FROM N.A.

RP STRAIN=Wistar; TISSUE=Liver;

RC MEDLINE=92329550; Pubmed=1627650;

RX Okaefuji T., Maekawa K., Nawa K., Marumoto Y.;

RA "The cDNA cloning and mRNA expression of rat protein C.;"

RT Biochem. Biophys. Acta 131:329-332(1992).

RL

CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.

CC

CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIIa.

CC

CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS STRONGLY PROMOTED BY THROMBOMODULIN.

CC

CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.

CC

CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME GUO RESIDUES ALONG THE MODIFIED PROTEIN TO BIND CALCIUM.

	-1-	MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING STATE IS NECESSARY FOR THE RECOGNITION OF THE THROMBIN-THROMBOMODULIN COMPLEX.
	-1	SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
	-1-	SIMILARITY: Contains 2 EGF-like domains.
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DR	EMBL; X64336;	CAA45617.1; .
DR	PIR; SI8994;	SI8994.
DR	HSSP; P04070;	IPCU.
DR	MEROPS; S01.218;	--
DR	InterPro; IPR000152;	Aex_hydroxyl_1.
DR	InterPro; IPR001314;	Chymotrypsin.
DR	InterPro; IPR001881;	BGF_Ca.
DR	InterPro; IPR006209;	BGF_like.
DR	InterPro; IPR002383;	Gla_blood.
DR	InterPro; IPR001254;	Ser_protease_Ty.
DR	InterPro; IPR000294;	Vltk_dep_gla.
DR	Pfam; PF00008;	EGF_1; 1.
DR	Pfam; PF00594;	Gla; 2.
DR	Pfam; PF00089;	Tryptsin; 1.
DR	PRINTS; PR00722;	CHYMOTRYPSIN.
DR	PRINTS; PR00001;	GLABLOOD.
DR	SMART; SMART0179;	EGF_CA; 1.
DR	SMART; SMART0069;	GLA; 1.
DR	SMART; SMART0020;	TRYP_SPEC; 1.
DR	PROSITE; PS00010;	ASX_HYDROXYL; 1.
DR	PROSITE; PS00022;	EGF_1; 1.
DR	PROSITE; PS01186;	EGF_2; 2.
DR	PROSITE; PS01187;	EGF_CA; 1.
DR	PROSITE; PS00011;	GUU_CARBOXYLATON; 1.
DR	PROSITE; PSS0240;	TRYP SIN_DOM; 1.
DR	PROSITE; PSS0134;	TRYP SIN_HIT; 1.
DR	PROSITE; PS00135;	TRYP SIN_SER; 1.
KW	Blood coagulation;	Glycoprotein; Serine protease;
KM	Gamma-carboxyglutamic acid;	Calcium-binding; Vitamin K; Hydroxylation,
KV	EGF-like domain; Repeat;	Endothelial cell; Hydrolase; Signal.
FT	SIGNAL	1..32
FT	PROPEP	33..41
FT	CHAIN	42..196
FT	CHAIN	199..461
FT	PERITIDE	199..212
FT	SITE	212..213
FT	DNAIIN	96..131
FT	DNAIIN	135..175
FT	DNAIIN	213..461
FT	MOD_RES	47..47
FT	MOD_RES	48..48
FT	MOD_RES	55..55
FT	MOD_RES	57..57
FT	MOD_RES	60..60
FT	MOD_RES	61..61
FT	MOD_RES	66..66
FT	MOD_RES	67..67
FT	MOD_RES	70..70
FT	MOD_RES	112..112

FT ACT\_SITE 254 254 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 300 300 CHARGE RELAY SYSTEM.  
 FT ACT\_SITE 402 402 CHARGE RELAY SYSTEM.  
 FT DISULFID 58 63 BY SIMILARITY.  
 FT DISULFID 91 110 BY SIMILARITY.  
 FT DISULFID 100 105 BY SIMILARITY.  
 FT DISULFID 104 119 BY SIMILARITY.  
 FT DISULFID 121 130 BY SIMILARITY.  
 FT DISULFID 139 150 BY SIMILARITY.  
 FT DISULFID 146 159 BY SIMILARITY.  
 FT DISULFID 161 174 BY SIMILARITY.  
 FT DISULFID 182 320 INTERCHAIN (BY SIMILARITY).  
 FT DISULFID 239 255 BY SIMILARITY.  
 FT DISULFID 373 387 BY SIMILARITY.  
 FT DISULFID 398 426 BY SIMILARITY.  
 FT CAROXYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROXYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROXYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 461 AA; 51912 MW; 844CF9364EDACD5 CRC64;

Query Match 52.6%; Score 100; DB 1; Length 461;  
 Best Local Similarity 45.5%; Pred. No. 2, 7e-10;  
 Matches 20; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFXXLRQSGLXKCKKXQCSFFXXRXIFDAXRTKLFWISY 44  
 Db 42 ANSFLEVRAGSLERECMEICDFEAOEIFQNVDTLAFWIKY 85

## RESULT 11

RA10\_RABIT STANDARD; PRT; 490 AA.  
 AC 019045;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 28-SEP-2003 (Rel. 41, Last annotation update)  
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).  
 GN F10.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_Taxid=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=97256311; PubMed=9101642;  
 RA Pendurthi U.R., Anderson K.D., James H.L.;  
 RT "Characterization of a full-length cDNA for rabbit factor X.";  
 RL Thromb. Res. 85:503-514(1997).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 converts prothrombin to thrombin in the presence of factor Va,  
 calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 MORE DISULFIDE BONDS.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMIC CARBOXYLATION OF SOME  
 GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CALCIUM (BY SIMILARITY).  
 CC -1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).  
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)  
 (BY SIMILARITY).  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 ANOTHER SITE, BEYOND THE GLA DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: Contains 2 EGF-like domains.  
 CC -----  
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 modified and this statement is not removed. Usage by and for commercial

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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: AF003200; AAB62542.1; -  
 DR HSSP: P0742; IHCG.  
 DR MEROPS: S01.216; -  
 DR InterPro: IPR000152; Axx\_hydroxyl.  
 DR InterPro: IPR001314; Chymotrypsin.  
 DR InterPro: IPR000742; EGF 2.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR001638; EGF\_T1.  
 DR InterPro: IPR006209; EGF\_Like.  
 DR InterPro: IPR002383; GLA\_Blood.  
 DR InterPro: IPR001254; Ser protease\_Try.  
 DR InterPro: IPR000294; Vltk\_dep\_GLA.  
 DR Pfam: PF00008; EGF; 2.  
 DR Pfam: PF00594; gla; 1.  
 DR Pfam: PF00089; Elypsin; 1.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR PRINTS: PR00010; EGFBLDOD.  
 DR PRINTS: PR00001; GLABLOOD.  
 DR SMART: SM00179; EGF\_CA; 1.  
 DR SMART: SM00069; GLA\_1.  
 DR SMART: SM00020; TYP\_Spc; 1.  
 DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE: PS00022; EGF\_1; 1.  
 DR PROSITE: PS01186; EGF\_2; 2.  
 DR PROSITE: PS01187; EGF\_CA; 1.  
 DR PROSITE: PS00011; GLU\_CARBOXYLATION; 1.  
 DR PROSITE: PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 DR Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;  
 KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;  
 KW Signal; Zymogen; EGF-like domain; Repeat.  
 FT SIGNAL 1 20  
 FT PROPEP 1 40  
 FT CHAIN 41 180  
 FT CHAIN 184 490  
 FT PROPEP 184 232  
 FT CHAIN 233 490  
 FT CHAIN 86 122  
 FT DOMAIN 125 165  
 FT DOMAIN 233 490  
 FT MOD\_RES 46 46  
 FT MOD\_RES 47 47  
 FT MOD\_RES 54 54  
 FT MOD\_RES 56 56  
 FT MOD\_RES 59 59  
 FT MOD\_RES 60 60  
 FT MOD\_RES 65 65  
 FT MOD\_RES 66 66  
 FT MOD\_RES 69 69  
 FT MOD\_RES 72 72  
 FT MOD\_RES 75 75  
 FT MOD\_RES 79 79  
 FT MOD\_RES 103 103  
 FT ACT\_SITE 274 274  
 FT ACT\_SITE 320 320  
 FT ACT\_SITE 417 417  
 FT DISULFID 90 101

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FT DISULFID 95 110 BY SIMILARITY.
FT DISULFID 112 121 BY SIMILARITY.
FT DISULFID 129 140 BY SIMILARITY.
FT DISULFID 136 149 BY SIMILARITY.
FT DISULFID 151 164 BY SIMILARITY.
FT DISULFID 172 340 INTERCHAIN (BY SIMILARITY).
FT DISULFID 239 244 BY SIMILARITY.
FT DISULFID 259 275 BY SIMILARITY.
FT DISULFID 388 402 BY SIMILARITY.
FT DISULFID 413 441 BY SIMILARITY.
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 490 AA, 53965 MW, 3A39FA85AF2A6D11 CRC64;

Query Match 52.6%; Score 100; DB 1; Length 490;
Best Local Similarity 40.9%; Pred. No. 2.9e-10;
Matches 18; Conservative 8; Mismatches 18; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRGSLRXCKXQCSFXAXRXIFKDXARTLFWISY 44
Db 41 ANSLLELKKNLRECKENCSIBELAVEDEKTEFWNKY 84

RESULT 12
FA10_CHICK STANDARD; PRT: 475 AA.
AC P2515;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor)
DE (Virus activating protease) (VAP).
GN FX
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Chorioallantoic membrane;
RX MEDLINE=91257322; PubMed=2044767;
RA Suzuki H., Harada A., Hayashi Y., Wada K., Asaka J.-I., Gotch B.,
RA Ogasawara T., Nagai Y.;
RT "Primary structure of the virus activating protease from chick
RT embryo. Its identity with the blood clotting factor Xa.";
RL FEBS Lett. 283:281-285(1991).
RN [2]
RP SEQUENCE OF 41-55 AND 241-261.
RC TISSUE=Allantoic fluid;
RX MEDLINE=91065352; PubMed=2174359;
RA Gotch B., Ogasawara T., Toyoda T., Innocencio N.M., Hamaguchi M.,
RA Nagai Y.;
RT "An endoprotease homologous to the blood clotting factor X as a
RT determinant of viral tropism in chick embryo.";
RL EMBO J. 9:4189-4195(1990).
CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that
CC converts prothrombin to thrombin in the presence of factor Va,
CC calcium and phospholipid during blood clotting.
CC -1- FUNCTION: VAP CLEAVES THE FUSION PROTEINS OF SENAI VIRUS, NDV,
CC AND INFLUENZA VIRUS A AT A SPECIFIC SINGLE ARGININE-CONTAINING
CC SITE, AND PLAYS A KEY ROLE IN THE VIRAL SPREADING IN THE ALLANTOIC
CC SAC.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then
CC Arg-|-Ile bonds in prothrombin to form thrombin.
CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR
CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR
CC MORE DISULFIDE BONDS.
CC -1- TISSUE SPECIFICITY: LIVER AND CHORIOALLANTOIC MEMBRANE.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND

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CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE
CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D00844; BA00724.1; -.
DR PIR: S15838; EXCH.
DR HSP: P00742; IHCG.
DR MEROPS: S01.216; -.
DR InterPro: IPR000152; Axx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_11.
DR InterPro: IPR006209; EGF_11k.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; Vltk_dep_GLA.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00594; GLA; 1.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00010; EGFBL00D.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA_1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TYP_SPC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolase; Serine protease; Plasma; Blood coagulation;
KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KW Signal; Zymogen; EGF-like domain; Repeat.
FT SIGNAL 1 20 OR 30, OR 31 (POTENTIAL).
FT PROPEP 21 40
FT CHAIN 41 180 FACTOR X LIGHT CHAIN.
FT CHAIN 186 475 FACTOR X HEAVY CHAIN.
FT PROPEP 186 241 ACTIVATION PEPTIDE.
FT CHAIN 242 475 ACTIVATED FACTOR XA, HEAVY CHAIN.
FT DOMAIN 86 122 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 125 168 EGF-LIKE 2.
FT DOMAIN 241 475 SERINE PROTEASE.
FT MOD_RES 46 46 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 47 47 (BY SIMILARITY).
FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 54 54 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 56 56 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 59 59 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 59 59 (BY SIMILARITY).
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 60 60 (BY SIMILARITY).
FT MOD_RES 65 65 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 65 65 (BY SIMILARITY).
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 66 66 (BY SIMILARITY).
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 69 69 (BY SIMILARITY).

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FT MOD_RES 72 72 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 79 79 (BY SIMILARITY).
FT MOD_RES 79 79 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 103 103 (BY SIMILARITY).
FT ACT_SITE 282 282 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 328 328 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 425 425 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 90 101 BY SIMILARITY.
FT DISULFID 95 110 BY SIMILARITY.
FT DISULFID 112 121 BY SIMILARITY.
FT DISULFID 129 140 BY SIMILARITY.
FT DISULFID 136 152 BY SIMILARITY.
FT DISULFID 154 167 BY SIMILARITY.
FT DISULFID 175 348 INTERCHAIN (BY SIMILARITY).
FT DISULFID 247 252 BY SIMILARITY.
FT DISULFID 267 283 BY SIMILARITY.
FT DISULFID 396 410 BY SIMILARITY.
FT DISULFID 421 449 BY SIMILARITY.
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 475 AA; 53142 MW; 570BF84956C5C74D CRC64;

Query Match 51.1%; Score 97; DB 1; Length 475;
Best Local Similarity 40.9%; Pred. No. 9.7e-10;
Matches 18; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

OY 1 ANAFIXLRGSLXRCCKXCKSCFXKXRIFFDAXRTKLFWTSY 44
Db 41 ANSFLEMKQGNIERECNEERCSKEAREAFDNEKTEEFMNY 84

RESULT 13
PRTC_BOVIN STANDARD; PRT; 456 AA.
ID P00745;
AC 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV) (Fragment).
DE PROC.
GN Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
OK NCBI_TaxID=9913;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=85014826; PubMed=6091100;
RA Long G.L., Balagaje R.M., McGillicrath R.T.A.;
RA "Cloning and sequencing of liver cDNA coding for bovine protein C.";
RA Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
RN (2)
RP SEQUENCE OF 40-194, AND CARBOHYDRATE-LINKAGE SITE ASN-136.
RX MEDLINE=83007325; PubMed=6896876;
RA Fernlund P., Stenflo U.;
RA "Amino acid sequence of the light chain of bovine protein C.";
RA J. Biol. Chem. 257:12170-12179(1982).
RN (3)
RP REVISION TO 110.
RX MEDLINE=83169769; PubMed=6572939;
RA Drakeberg T., Fernlund P., Roesporoff P., Stenflo U.;
RA "Beta-hydroxyaspartic acid in vitamin K-dependent protein C.";
RA Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
RN (4)
RP SEQUENCE OF 197-456, AND CARBOHYDRATE-LINKAGE SITES ASN-269; ASN-350
RP AND ASN-366.
RX MEDLINE=83007326; PubMed=6896877;
RA Stenflo U., Fernlund P.;
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RT "Amino acid sequence of the heavy chain of bovine protein C.";
RL J. Biol. Chem. 257:12180-12190(1982).
RN (5)
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213513; PubMed=6904092;
RA Esmon N.L., Debault L.E., Esmon C.T.;
RA "Proteolytic formation and properties of gamma-carboxylglutamic acid-
RA domainless protein C.";
RL J. Biol. Chem. 258:5548-5553(1983).
RN (6)
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213514; PubMed=6406503;
RA Johnson A.E., Esmon N.L., Laue T.M., Esmon C.T.;
RA "Structural changes required for activation of protein C are induced
RA by Ca2+ binding to a high affinity site that does not contain gamma-
RA carboxylglutamic acid.";
RL J. Biol. Chem. 258:5554-5560(1983).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMOLOGIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -----
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CC -----
DR EMBL; K02435; AAA30685.1; -.
DR PIR; A26250; KXBO.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002183; GLA_Blood.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
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DR PROSITE; PS00135; TRYPSIN SER; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
FT NON_TER 1 1
FT SIGNAL <1 29
FT PROPER 30 39
FT CHAIN 40 194
FT CHAIN 197 456
FT PEPTIDE 197 210
FT DOMAIN 94 129
FT DOMAIN 133 173
FT DOMAIN 211 456
FT MOD_RES 45 45
FT MOD_RES 46 46
FT MOD_RES 53 53
FT MOD_RES 55 55
FT MOD_RES 58 58
FT MOD_RES 59 59
FT MOD_RES 62 62
FT MOD_RES 64 64
FT MOD_RES 65 65
FT MOD_RES 68 68
FT MOD_RES 74 74
FT MOD_RES 110 110
FT ACT_SITE 252 252
FT ACT_SITE 298 298
FT ACT_SITE 397 397
FT ACT_SITE 56 61
FT DISULFID 89 108
FT DISULFID 98 103
FT DISULFID 102 117
FT DISULFID 119 128
FT DISULFID 137 148
FT DISULFID 144 157
FT DISULFID 159 172
FT DISULFID 180 318
FT DISULFID 237 253
FT DISULFID 368 382
FT DISULFID 393 421
FT CARBOHYD 136 136
FT CARBOHYD 289 289
FT CARBOHYD 350 350
FT CARBOHYD 366 366
FT VARIANT 82 82
FT CONFLICT 455 456
SQ SEQUENCE 456 AA; 51407 MW; CNAF633F894C209 CRC64;

Query Match 50.5%; Score 96; DB 1; Length 456;
Best Local Similarity 43.2%; Pred. No. 1.4e-09;
Matches 19; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRQSLKRXCKXQCSFYXARXIFPKDAXRTKLFWISY 44
Db 40 ANSFLEELRPQNVRECESEVEFEAREEIFONTEDTIAFWFSFY 83

RESULT 14
TMG3 HUMAN STANDARD; PRT; 231 AA.
AC Q9B2D7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transmembrane gamma-carboxyglutamic acid protein 3 precursor.
GN TMG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spinal cord;

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RX MEDLINE=21117044; PubMed=11171957;
RA Kujala J.D., Harris J.E., Xie L., Davie E.W.;
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
RT proteins expressed broadly in fetal and adult tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.
CC -1- PTM: Gla residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
CC -----
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CC -----
DR EMBL; AF326350; AAK00955.1; -.
DR HSSP; P00740; ICFH.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPER 1 19
FT CHAIN 20 231
FT FT 19 POTENTIAL.
FT FT 20 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT FT 78 PROTEIN 3.
FT FT 79 EXTRACELLULAR (POTENTIAL).
FT FT 101 POTENTIAL.
FT FT 102 CYTOPLASMIC (POTENTIAL).
FT FT 23 GLA-RICH.
FT FT 60
FT FT 231
SQ SEQUENCE 231 AA; 25848 MW; 8A373E48490D81 CRC64;

Query Match 49.5%; Score 94; DB 1; Length 231;
Best Local Similarity 38.6%; Pred. No. 1.6e-09;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Oy 1 ANAFLLXLRQSLKRXCKXQCSFYXARXIFPKDAXRTKLFWISY 44
Db 20 ANSFLEELRPQNVRECESEVEFEAREEIFONTEDTIAFWFSFY 63

RESULT 15
FA9 HUMAN STANDARD; PRT; 461 AA.
ID FA9 HUMAN
AC P00740;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Coagulation factor IX precursor (EC 3.4.21.22) (Christmas factor).
GN F9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86000558; PubMed=2994716;
RA Yoshitake S., Schach B.G., Foster D.C., Davie E.W., Kurachi K.;
RT "Nucleotide sequence of the gene for human factor IX (antihemophilic
RT factor B).";
RL Biochemistry 24:3736-3750(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85190593; PubMed=3857619;
RA McGraw R.A., Davis L.M., Noyes C.M., Lundblad R.L., Roberts H.R.,
RA Graham U.B., Stafford D.W.;
RT "Evidence for a prevalent dimorphism in the activation peptide of
RT human coagulation factor IX.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:2847-2851(1985).

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[13] SEQUENCE FROM N.A.  
RX MEDLINE=84236100; PubMed=6329734;  
RA Anson D.S., Choo K.H., Rees D.J.G., Giannelli F., Gould K.G.,  
RA Huddleston J.A., Brownlee G.G.;  
RT "The gene structure of human anti-haemophilic factor IX";  
RL EMBO J. 3:1053-1060(1984).  
[14] SEQUENCE FROM N.A.  
RX MEDLINE=8320788; PubMed=6687940;  
RA Jave M., de la Salle H., Schamber F., Bolland A., Kohli V.,  
RA Pinelli A., Tolstoshev P., Lecocq J.P.;  
RT "Isolation of a human anti-haemophilic factor IX cDNA clone using a  
RT unique 52-base synthetic oligonucleotide probe deduced from the amino  
RT acid sequence of bovine factor IX";  
RL Nucleic Acids Res. 11:2325-2335(1983).  
[15] SEQUENCE FROM N.A., AND VARIANTS THR-194 AND PRO-461.  
RA Rieder M.U., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,  
RA Rajkumar N.R., Toch E.J., Yi Q., Nickerson D.A.;  
RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.  
[16] SEQUENCE OF 36-326 FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=8430526; PubMed=6089357;  
RA Jagadeeswaran P., Lavelle D.E., Kaul R., Mohandas T., Warren S.T.;  
RT "Isolation and characterization of human factor IX cDNA:  
RT identification of Tag I polymorphism and regional assignment";  
RL Somat. Cell Mol. Genet. 10:465-473(1984).  
[17] SEQUENCE OF 290-359 FROM N.A.  
RX MEDLINE=88127096; PubMed=3340825;  
RA Stotler E.S., Koebel D.D., Sarkar G., Sommer S.S.;  
RT "Genomic amplification with transcript sequencing";  
RL Science 239:491-494(1988).  
[18] SEQUENCE OF 444-461 FROM N.A.  
RX MEDLINE=94054330; PubMed=826150;  
RA de la Salle C., Charantier J.L., Baas M.J., Schwartz A.,  
RA Wiesel M.L., Grunebaum L., Cazenave J.-P.;  
RT "A deletion located in the 3' non translated part of the factor IX  
RT gene responsible for mild haemophilia B";  
RL Thromb. Haemost. 70:370-371(1993).  
[19] SEQUENCE OF 47-461 (VARIANT NAGoya).  
RX MEDLINE=90078229; PubMed=2592373;  
RA Suehiro K., Kawabata S.-I., Miyata T., Takeya H., Takamatsu J.,  
RA Ogata K., Kamaya T., Saito H., Nino Y., Iwanaga S.;  
RT "Blood clotting factor IX BM Nagoya. Substitution of arginine 180 by  
RT tryptophan and its activation by alpha-chymotrypsin and rat mast cell  
RT chymase";  
RL J. Biol. Chem. 264:21257-21265(1989).  
[10] HYDROXYLATION OF ASP-110.  
RX MEDLINE=83308813; PubMed=6688526;  
RA McMullen B.A., Fujikawa K., Kisiel W.;  
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin  
RT K-dependent blood coagulation zymogens";  
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).  
[11] PROCESSING, ACTIVE SITE, AND CARBOHYDRATE-LINKAGE SITES.  
RX MEDLINE=78194509; PubMed=659613;  
RA di Scipio R.G., Kurachi K., Davie E.W.;  
RT "Activation of human factor IX (Christmas factor)";  
RL J. Clin. Invest. 61:1528-1538(1978).  
[12] CALCIUM-BINDING DATA.  
RX MEDLINE=84185715; PubMed=6425296;  
RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;  
RT "Derivatives of blood coagulation factor IX contain a high affinity  
RT Ca2+-binding site that lacks gamma-carboxyglutamic acid";  
RL J. Biol. Chem. 259:5698-5704(1984).  
[13]

RP ERRATUM.  
RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;  
RL J. Biol. Chem. 260:2583-2583(1985).  
[14] SIGNAL SEQUENCE CLEAVAGE SITE  
RX MEDLINE=86189947; PubMed=3009023;  
RA Bentley A.K., Rees D.J.G., Rizza C., Brownlee G.G.;  
RT "Defective propeptide processing of blood clotting factor IX caused  
RT by mutation of arginine to glutamine at position -4";  
RL Cell 45:343-348(1986).  
[15] STRUCTURE OF CARBOHYDRATE ON SER-99.  
RX MEDLINE=90062160; PubMed=2511201;  
RA Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T., Takao T.,  
RA Shimonishi Y., Iwanaga S.;  
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide  
RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first  
RT epidermal growth factor-like domain of human factors VII and IX and  
RT protein Z and bovine protein Z";  
RL J. Biol. Chem. 264:20320-20325(1989).  
[16] STRUCTURE OF CARBOHYDRATE ON SER-99.  
RX MEDLINE=91344709; PubMed=2129367;  
RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;  
RT "A new trisaccharide sugar chain linked to a serine residue in the  
RT first EGF-like domain of clotting factors VII and IX and protein Z";  
RL Adv. Exp. Med. Biol. 281:121-131(1990).  
[17] STRUCTURE OF CARBOHYDRATE ON SER-107.  
RX MEDLINE=92388094; PubMed=1517205;  
RA Nishimura H., Takao T., Hase S., Shimonishi Y., Iwanaga S.;  
RT "Human factor IX has a tetrasaccharide O-glycosidically linked to  
RT serine 61 through the fucose residue";  
RL J. Biol. Chem. 267:17520-17525(1992).  
[18] PHOSPHORYLATION OF SER-114.  
RX Harris R.J., Papac D.I., Tuong L., Smith K.J.;  
RT "Partial phosphorylation of serine-68 in EGF-1 of human factor IX";  
RL (In) Abstracts of Xth international conference on methods in protein  
RL structure analysis, pp.50-50, Annecy (1996).  
[19] POST-TRANSLATIONAL MODIFICATIONS.  
RX MEDLINE=20575397; PubMed=11133752;  
RA Arruda V.R., Hagstrom J.N., Deltch J., Helman-Patterson T.,  
RA Camire R.M., Chu K., Fields P.A., Herzog R.W., Couto L.B.,  
RA Larson P.J., High K.A.;  
RT "Posttranslational modifications of recombinant myotube-synthesized  
RT human factor IX";  
RL Blood 97:130-138(2001).  
[20] STRUCTURE BY NMR OF 47-93.  
RX MEDLINE=95229607; PubMed=7713897;  
RA Freedman S.J., Furtle B.C., Furtle B., Baleja J.D.;  
RT "Structure of the metal-free gamma-carboxyglutamic acid-rich membrane  
RT binding region of factor IX by two-dimensional NMR spectroscopy";  
RL J. Biol. Chem. 270:7980-7987(1995).  
[21] STRUCTURE BY NMR OF 47-93.  
RX MEDLINE=96032604; PubMed=7547952;  
RA Freedman S.J., Furtle B.C., Furtle B., Baleja J.D.;  
RT "Structure of the calcium ion-bound gamma-carboxyglutamic acid-rich  
RT domain of factor IX";  
RL Biochemistry 34:12126-12137(1995).  
[22] STRUCTURE BY NMR OF 47-93.  
RX MEDLINE=96279169; PubMed=8663165;  
RA Freedman S.J., Blostein M.D., Baleja J.D., Jacobs M., Furtle B.C.,  
RA Furtle B.;  
RT "Identification of the phospholipid binding site in the vitamin K-  
RT dependent blood coagulation protein factor IX";  
RL J. Biol. Chem. 271:16227-16236(1996).  
[23] STRUCTURE BY NMR OF 47-93.  
RP



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OM protein - protein search, using sw model

Run on: July 28, 2003, 12:21:25 ; Search time 61 Seconds  
(without alignments)  
186.136 Million cell updates/sec

Title: SEQ3  
Sequence: 1 ANAFIXLRGSLRXCKXX.....XXARXIFKDXRTLFWISY 44

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues  
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	164	86.3	701	Q96P08	Q96P08 homo sapien
2	119	62.6	446	1 Q61109	Q61109 mus musculu
3	105	55.3	268	4 Q8NEK6	Q8NEK6 homo sapien
4	105	55.3	446	1 Q8K3U6	Q8K3U6 ratu
5	102	53.7	443	13 Q8JH36	Q8JH36 brachyd
6	101	53.2	460	11 Q91WN8	Q91WN8 mus musculu
7	98	51.6	229	13 Q8JH40	Q8JH40 xenopus lae
8	98	51.6	482	11 Q63207	Q63207 ratu
9	96	50.5	469	6 Q9GMD9	Q9GMD9 ornithorhyn
10	96	50.5	481	11 Q54740	Q54740 mus musculu
11	96	50.5	481	11 Q99L32	Q99L32 mus musculu
12	96	50.5	481	11 Q88947	Q88947 mus musculu
13	95	50.0	460	11 Q99P06	Q99P06 mus musculu
14	94	49.5	231	4 Q8NZN6	Q8NZN6 homo sapien
15	93	48.9	456	6 Q9TTR0	Q9TTR0 canis famli
16	88	46.3	456	4 Q14316	Q14316 homo sapien

17	88	46.3	461	6 Q95ND7	Q95ND7 pan troglod
18	88	46.3	461	6 Q95ND6	Q95ND6 pan troglod
19	88	46.3	474	13 Q8JHC8	Q8JHC8 brachyd
20	87	45.8	49	6 Q95ME8	Q95ME8 bos taurus
21	85	44.7	100	4 Q15253	Q15253 homo sapien
22	82	43.2	376	13 P83370	P83370 homiocephal
23	81	42.6	179	4 Q8TAS3	Q8TAS3 homo sapien
24	81	42.6	198	11 Q8R182	Q8R182 mus musculu
25	80	42.1	138	6 Q28994	Q28994 sus scrofa
26	75	39.5	433	13 Q8JHD0	Q8JHD0 brachyd
27	75	39.5	433	13 Q90TK1	Q90TK1 brachyd
28	75	39.5	648	6 Q29094	Q29094 sus scrofa
29	72	37.9	55	4 Q8J002	Q8J002 homo sapien
30	72	37.9	55	4 Q8IXB5	Q8IXB5 homo sapien
31	72	37.9	399	11 Q8C101	Q8C101 mus musculu
32	72	37.9	399	11 Q9C0M3	Q9C0M3 mus musculu
33	70	36.8	98	13 P82807	P82807 notechis sc
34	70	36.8	650	4 Q16519	Q16519 homo sapien
35	70	36.8	650	4 Q9NSD0	Q9NSD0 homo sapien
36	65.5	34.5	542	5 Q8T613	Q8T613 halocynthia
37	64.5	33.9	226	11 Q8BM25	Q8BM25 mus musculu
38	64.5	33.9	226	11 Q8BGN6	Q8BGN6 mus musculu
39	63.5	33.4	431	10 Q94EY5	Q94EY5 arabidopsis
40	63.5	33.4	492	10 Q9SMJ7	Q9SMJ7 cicier ariet
41	63.5	33.4	543	10 Q9MB23	Q9MB23 arabidopsis
42	63.5	33.4	576	10 Q9C9U4	Q9C9U4 arabidopsis
43	63.5	33.4	589	10 Q9LMS2	Q9LMS2 arabidopsis
44	63	33.2	503	13 Q8AYE4	Q8AYE4 brachyd
45	63	33.2	608	13 Q9PTW7	Q9PTW7 struthio ca

## ALIGNMENTS

RESULT 1

Q96P08	PRELIMINARY;	PRT;	701 AA.
ID	Q96P08		
AC	Q96P08		
DT	01-DEC-2001 (TRENDS)		
DT	01-DEC-2001 (TRENDS)		
DT	01-MAR-2003 (TRENDS)		
DE	Factor VII active site mutant immunocognate.		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_Taxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21477448; PubMed=11593034;		
RT	Hu Z., Garen A.;		
RT	"Targeting tissue factor on tumor vascular endothelial cells and tumor		
RT	cells for immunotherapy in mouse models of prostatic cancer.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).		
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.		
DR	EMBL; AF272774; AKS58686.1; -		
DR	HGSP; P00761; IAN1.		
DR	InterPro; IPR000152; Asx_hydroxyl.		
DR	InterPro; IPR001314; Chymotrypsin.		
DR	InterPro; IPR000742; BGF_2.		
DR	InterPro; IPR001881; BGF_Ca.		
DR	InterPro; IPR001438; BGF_II.		
DR	InterPro; IPR006209; BGF_III.		
DR	InterPro; IPR002383; GLA_blood.		
DR	InterPro; IPR007110; IG_1like.		
DR	InterPro; IPR003597; IG_2like.		
DR	InterPro; IPR003006; IG_MHC.		
DR	InterPro; IPR001254; Ser_protease_Try.		
DR	InterPro; IPR000294; VitK_dep_GLA.		
DR	Pfam; PF00008; BGF_2.		
DR	Pfam; PF00594; G1a; 1.		
DR	Pfam; PF00047; IG; 2.		
DR	Pfam; PF00089; trypsin; 1.		
DR	PRINTS; PR00722; CHYMOTRYPSIN.		

DR PRINTS; PR00010; EGFBL00D.  
DR PRINTS; PR00001; GLABLO0D.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00407; IGCL; 1.  
DR SMART; SM00020; TRYSPC; 1.  
DR PROSITE; PS00010; ASK\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS50835; IG\_Like; 2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
DR EGF-like domain; Hydroxylase; Protease; Serine protease.  
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CB42CC992F CRC64;

Query Match 86.3%; Score 164; DB 4; Length 701;  
Best Local Similarity 75.0%; Pred. No. 76-22;  
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGSILRXCKXQCSFXAXRIFKDAKRTKLFWISY 44  
DB 61 ANAFLELRPGSLERCKEKGCSFEAREIFKDAERTKLFWISY 104

## RESULT 2

ID 061109 PRELIMINARY; PRT; 446 AA.  
AC 061109;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Coagulation factor VII.  
CN P7 OR FVII.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=96376538; PubMed=8701412;  
RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,  
RA Castellino F.J.;  
RT "Characterization of a cDNA encoding murine coagulation factor VII.",  
RL Thromb. Haemost. 75:481-487(1996).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
DR EMBL; U44795; AAC52570.1; -.  
DR HSSP; P08709; 1PAK.  
DR MGD; MGI:109325; F7.  
DR InterPro; IPR002086; Aldehyde\_dehydr.  
DR InterPro; IPR00152; Asx\_hydroxyl.  
DR InterPro; IPR00134; Chymotrypsin.  
DR InterPro; IPR001064; Crystallin.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_Like.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR001254; Set\_protease\_Try.  
DR InterPro; IPR00294; VitK\_dep\_GLA.  
DR Pfam; PF00594; gla; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00001; GLABLO0D.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00020; TRYSPC; 1.  
DR PROSITE; PS00070; ALDEHYDE\_DEHYDR\_CYS; 1.  
DR PROSITE; PS00010; ASK\_HYDROXYL; 1.  
DR PROSITE; PS00225; CRYSTALLIN\_BETA; 1.  
RT

DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
DR EGF-like domain; Hydroxylase; Protease; Serine protease.  
SQ SEQUENCE 446 AA; 50318 MW; 482FD09B8F5D6870 CRC64;

Query Match 62.6%; Score 119; DB 11; Length 446;  
Best Local Similarity 56.8%; Pred. No. 1.2e-13;  
Matches 25; Conservative 1; Mismatches 18; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGSILRXCKXQCSFXAXRIFKDAKRTKLFWISY 44  
DB 42 ANSLLEELMPGSLERCKEKGCSFEAREIFKSPERTKQFIVY 85

## RESULT 3

ID 08NEK6 PRELIMINARY; PRT; 268 AA.  
AC 08NEK6;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Proline-rich Gla (G-carboxyglutamic acid) polypeptide 1  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RA Strauberg R.;  
RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC030786; AAH30786.1; -.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR00294; VitK\_dep\_GLA.  
DR Pfam; PF00594; gla; 1.  
DR PRINTS; PR00001; GLABLO0D.  
DR SMART; SM00069; GLA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
FT NON\_TER 1  
SQ SEQUENCE 268 AA; 30295 MW; C3A47C2D90007739 CRC64;

Query Match 55.3%; Score 105; DB 4; Length 268;  
Best Local Similarity 43.2%; Pred. No. 3.1e-11;  
Matches 19; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGSILRXCKXQCSFXAXRIFKDAKRTKLFWISY 44  
DB 71 ANGFEEIRQNIIECKEKECTFEAREARENNKEKTEFWISY 114

## RESULT 4

ID 08K3U6 PRELIMINARY; PRT; 446 AA.  
AC 08K3U6;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Coagulation factor VII.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RA Murphy K., Ramaker M.;  
RT "Nucleotide sequence of the cDNA encoding rat coagulation factor VII.",  
RT







DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00020; TRYP\_SPC; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
DR EGF-like domain; Hydrolase; Protease; Serine protease.  
SQ SEQUENCE 469 AA; 52196 MW; 4C66C230D0758F6A CRC64;

Query Match 50.5%; Score 96; DB 6; Length 469;  
Best Local Similarity 38.6%; Pred. No. 2.7e-09;  
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLRXCKXQCSFXARXIFKDXRTKLPWISY 44  
Db 41 ANSLFEEFKGNLERECNEETCSYEAREVEDTDKTNEFWNTY 84

RESULT 10  
ID 054740 PRELIMINARY; PRT; 481 AA.  
AC 054740;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Coagulation factor X precursor (EC 3.4.21.6).  
GN F10 OR F10.  
OS Mus musculus (Mouse).  
OC Plasmid plasmid.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=98454993; PubMed=9783672;  
RA Heidmann H.H., Kontermann R.B.;  
RT "Cloning and recombinant expression of mouse coagulation factor X";  
RU Thromb. Res. 92:33-41(1998).  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
DR EMBL; AJ222677; CAI0933.1; -.  
DR HSSP; P00742; IYKA.  
DR MEROPS; S01.216; -.  
DR MGD; MGI:103107; F10.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_CA.  
DR InterPro; IPR00438; EGF\_II.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VltK\_dep\_GLA.  
DR Pfam; PF00008; EGF; 1.  
DR Pfam; PF00594; GLA; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00010; EGF\_blood.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00020; TRYP\_SPC; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 2.

DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
DR EGF-like domain; Hydrolase; Protease; Serine protease; Signal;  
KW Plasmid.  
FT SIGNAL 1 40 POTENTIAL.  
FT CHAIN 41 481 COAGULATION FACTOR X.  
SQ SEQUENCE 481 AA; 53986 MW; CF702D5EFPD97AE CRC64;

Query Match 50.5%; Score 96; DB 11; Length 481;  
Best Local Similarity 38.6%; Pred. No. 2.8e-09;  
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLRXCKXQCSFXARXIFKDXRTKLPWISY 44  
Db 41 ANSLFEEFKGNLERECNEETCSYEAREVEDTDKTNEFWNTY 84

RESULT 11  
ID 099L32 PRELIMINARY; PRT; 481 AA.  
AC 099L32;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Coagulation factor X.  
GN F10.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strauberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
DR EMBL; BC003877; AA003877.1; -.  
DR HSSP; P00742; IYKA.  
DR MEROPS; S01.216; -.  
DR MGD; MGI:103107; F10.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_CA.  
DR InterPro; IPR00438; EGF\_II.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VltK\_dep\_GLA.  
DR Pfam; PF00008; EGF; 2.  
DR Pfam; PF00594; GLA; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00010; EGF\_blood.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00020; TRYP\_SPC; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
DR EGF-like domain; Hydrolase; Protease; Serine protease.  
KW SEQUENCE 481 AA; 54004 MW; BD88B96C8A0B7E7F CRC64;

Query Match 50.5%; Score 96; DB 11; Length 481;  
Best Local Similarity 38.6%; Pred. No. 2.8e-09;

	Matches	17;	Conservative	8;	Mismatches	19;	Indels	0;	Gaps	0																																		
QY	1	A	N	A	F	L	X	T	R	O	S	L	K	R	C	K	X	X	O	C	S	F	F	X	A	X	I	E	P	D	A	R	T	K	L	F	M	S	Y	44				
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:				
Db	41	A	N	S	F	F	E	E	F	K	G	N	L	E	R	E	C	M	E	I	C	S	Y	E	V	N	D	E	I	F	F	D	D	E	K	T	E	H	Y	M	T	K	Y	84

RESULT 12  
O88947

ID	088947	PRELIMINARY;	PRT;	481 AA.
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Query Match\* 50.5%; Score 96; DB 11; Length 481;

Query	Match	Score	DB	Length
1	01-NOV-1998 (TrEMBL)	96	11	481
2	01-NOV-1998 (TrEMBL)	96	11	481
3	01-MAR-2003 (TrEMBL)	96	11	481
4	01-MAR-2003 (TrEMBL)	96	11	481
5	01-MAR-2003 (TrEMBL)	96	11	481
6	01-MAR-2003 (TrEMBL)	96	11	481
7	01-MAR-2003 (TrEMBL)	96	11	481
8	01-MAR-2003 (TrEMBL)	96	11	481
9	01-MAR-2003 (TrEMBL)	96	11	481
10	01-MAR-2003 (TrEMBL)	96	11	481
11	01-MAR-2003 (TrEMBL)	96	11	481
12	01-MAR-2003 (TrEMBL)	96	11	481
13	01-MAR-2003 (TrEMBL)	96	11	481
14	01-MAR-2003 (TrEMBL)	96	11	481
15	01-MAR-2003 (TrEMBL)	96	11	481
16	01-MAR-2003 (TrEMBL)	96	11	481
17	01-MAR-2003 (TrEMBL)	96	11	481
18	01-MAR-2003 (TrEMBL)	96	11	481
19	01-MAR-2003 (TrEMBL)	96	11	481
20	01-MAR-2003 (TrEMBL)	96	11	481
21	01-MAR-2003 (TrEMBL)	96	11	481
22	01-MAR-2003 (TrEMBL)	96	11	481
23	01-MAR-2003 (TrEMBL)	96	11	481
24	01-MAR-2003 (TrEMBL)	96	11	481
25	01-MAR-2003 (TrEMBL)	96	11	481
26	01-MAR-2003 (TrEMBL)	96	11	481
27	01-MAR-2003 (TrEMBL)	96	11	481
28	01-MAR-2003 (TrEMBL)	96	11	481
29	01-MAR-2003 (TrEMBL)	96	11	481
30	01-MAR-2003 (TrEMBL)	96	11	481
31	01-MAR-2003 (TrEMBL)	96	11	481
32	01-MAR-2003 (TrEMBL)	96	11	481
33	01-MAR-2003 (TrEMBL)	96	11	481
34	01-MAR-2003 (TrEMBL)	96	11	481
35	01-MAR-2003 (TrEMBL)	96	11	481
36	01-MAR-2003 (TrEMBL)	96	11	481
37	01-MAR-2003 (TrEMBL)	96	11	481
38	01-MAR-2003 (TrEMBL)	96	11	481
39	01-MAR-2003 (TrEMBL)	96	11	481
40	01-MAR-2003 (TrEMBL)	96	11	481
41	01-MAR-2003 (TrEMBL)	96	11	481
42	01-MAR-2003 (TrEMBL)	96	11	481
43	01-MAR-2003 (TrEMBL)	96	11	481
44	01-MAR-2003 (TrEMBL)	96	11	481
45	01-MAR-2003 (TrEMBL)	96	11	481
46	01-MAR-2003 (TrEMBL)	96	11	481
47	01-MAR-2003 (TrEMBL)	96	11	481
48	01-MAR-2003 (TrEMBL)	96	11	481
49	01-MAR-2003 (TrEMBL)	96	11	481
50	01-MAR-2003 (TrEMBL)	96	11	481

Best Local Similarity 38.6%; Pred. No. 2.8e-09;  
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

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Oy      1 ANAEFLXLRQGS LXRXCXXXQCSFXXARXIFKDAYRTKLFWISY 44
         ||::|||::|||::|||::|||::|||
Db      41 ANSFEFEFKGNLRECEMBEICSYYEVRREIFEDDEKTYEWTKY 84

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### RESULT 13

ID Q99PC6 PRELIMINARY; PRT; 460 AA.

DT	01-JUN-2001	(Tremblrel. 17, Created)
DT	01-JUN-2001	(Tremblrel. 17, Last sequence update)
DT	01-MAR-2003	(Tremblrel. 23, Last annotation update)
DE	Anticoagulant protein C.	
GN	PROC.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL;	
RA	Korf I.;	
RT	"Complete sequence of UC72A01."	
RL	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.	
CC	-1- SIMILARITY: BELONGS TO THE EMBL/GenBank/DBJ databases.	
DR	EMBL; AF318182; AAK07918.1; -	
DR	HSSP; P04070; IAU.	
DR	MED; MG1:97771; Proc.	
DR	InterPro; IPR000152; Ser_protease_Try.	
DR	InterPro; IPR001314; Chymotrypsin.	
DR	InterPro; IPR001881; EGF_Ca.	
DR	InterPro; IPR006209; EGF_like.	
DR	InterPro; IPR002383; GLA_dlood.	
DR	InterPro; IPR001254; Ser_protease_Try.	
DR	InterPro; IPR00294; Vlek_dep_GLA.	
DR	Pfam; PF00008; EGF; 2.	
DR	Pfam; PF00594; Gla; 1.	
DR	Pfam; PF00089; trypsin; 1.	
DR	PRINTS; PR00722; CHYMOTRYPSIN.	
DR	PRINTS; PR00001; GLABLOOD.	
DR	SMART; SM00179; EGF_CA; 1.	
DR	SMART; SM00069; GLA; 1.	
DR	SMART; SM00020; Tryp_Spc; 1.	
DR	PROSITE; PS00010; ASX_HYDROXYL; 1.	
DR	PROSITE; PS00022; EGF_1; 1.	
DR	PROSITE; PS01186; EGF_2; 2.	
DR	PROSITE; PS01187; EGF_CA; 1.	
DR	PROSITE; PS00011; GLU_CARBOXYLATION; 1.	
DR	PROSITE; PS02040; TRYPSIN_DOM; 1.	
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.	
DR	PROSITE; PS00135; TRYPSIN_SER; 1.	
DR	EGF-like domain; Hydrolase; Protease; Serine protease.	
KW	EGF-like domain; Hydrolase; Protease; Serine protease.	
QW	SEQUENCE 460 AA; 51784 MW; 0293BC25B9D3ED16 CRC64;	
QY	Query Match 50.0%; Score 95; DB 11; Length 460;	
Db	Best Local Similarity 43.2%; Pred. No. 4.1e-09;	
	Matches 19; Conservative 5; Mismatches 20; Indels 0; Gaps 0;	
1	ANAEFLXLRQGSILRCKXXQCSFXKXRIFKDAXRTKLFWISY 44	
42	ANSFLEMRPGSLRERCMEEIFCDLEBAQEIFQVNEDTLAWIKY 85	
RESULT 14		
Q8N2N6		
Q8N2N6	PRELIMINARY;	PRT; 231 AA.
Q8N2N6		
DT	01-OCT-2002	(Tremblrel. 22, Created)
DT	01-OCT-2002	(Tremblrel. 22, Last sequence update)
DT	01-MAR-2003	(Tremblrel. 23, Last annotation update)

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DE Hypothetical protein FLJ90093.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Isegai T., Oca T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuko Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK074574; BAC11069.1; -
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR000294; VltK_dep_GLA.
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00069; GLA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
KW Hypothetical protein.
SQ SEQUENCE 231 AA; 25944 MW; 8A373B0D5C1D0D81 CRC64;

Query Match 49.5%; Score 94; DB 4; Length 231;
Best Local Similarity 38.6%; Pred. No. 3.1e-09;
Matches 17; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRQSLRXCKXXQCSFXKXIFKDAKRTKLFWISY 44
Db 20 ANEFLLELRQCTIERECMEICSYEVKVEVENKEMEFKGY 63

RESULT 15
Q9TTR0 PRELIMINARY; PRT; 456 AA.
AC Q9TTR0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Protein C precursor.
GN PROC.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_taxid=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Leeb T., Kopp T., Deppe A., Breen M., Matie U., Brunberg L.,
RA Brenig B.;
RT "Molecular characterization and chromosomal assignment of the canine
RL Mamm. Genome 10:135-139(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9371952; PubMed=10443005;
RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Brenig B.;
RT "Analysis of canine protein C gene polymorphisms.";
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL: AJ001979; CAA05126.1; -
DR HSP: P04070; IAT.
DR InterPro: IPR000152; Aex_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VltK_dep_GLA.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF00594; gla; 1.

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DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00181; EGF; 2.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; Tryp_SPC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolyase; Protease; Serine protease; Signal.
FT SIGNAL 1 42
FT CHAIN 43 192
FT CHAIN 193 194
FT CHAIN 195 456
SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59FF CRC64;

Query Match 48.9%; Score 93; DB 6; Length 456;
Best Local Similarity 40.9%; Pred. No. 9.5e-09;
Matches 18; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRQSLRXCKXXQCSFXKXIFKDAKRTKLFWISY 44
Db 43 ANSFLLELRQSLRXCKXXQCSFXKXIFKDAKRTKLFWISY 86

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Search completed: July 28, 2003, 12:27:33  
 Job time : 61 secs

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XX	WP1; 1999-288309/24.
DR	Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX	acid domain, useful for treating clotting disorders
PT	Disclosure; Page 80; 86pp; English.
XX	This sequence represents a modified GLA (gamma-carboxyglutamic acid)
XX	domain. The invention relates to a vitamin K-dependent polypeptide
CC	comprising a modified GLA domain containing an amino acid substitution
CC	which enhances membrane binding of the modified polypeptide as compared
CC	to the native polypeptide. The polypeptide is used to treat a clotting
CC	disorder by decreasing or increasing clot formation. Modification of the
CC	GLA domain results in a protein which has enhanced membrane binding
CC	affinity as compared to the native protein.
SQ	Sequence 44 AA;
QY	Query Match 87.9%; Score 167; DB 20; Length 44;
Db	Best Local Similarity 97.7%; Pred. No. 2.5e-21;
	Matches 43; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
	1 ANAFLLXLRGSLRXCKXKCSFYXARXIFPDAXRTKLFWTSY 44
	1 ANAFLLXLRGSLRXCKXKCSFYXARXIFPDAXRTKLFWTSY 44
RESULT 2	
ID	AA18302
ID	AA18302 standard; peptide; 44 AA.
AC	AA18302;
DT	17-AUG-1999 (first entry)
DE	Modified GLA domain of vitamin K-dependent protein.
KW	GLA domain; muten; vitamin K-dependent protein; clotting disorder;
KW	therapy.
OS	Homo sapiens.
OS	Synthetic.
XX	Key Location/Qualifiers
FT	Misc-difference 1..44
FT	/note= "Xaa= Gamma-carboxyglutamic acid, or glutamic
FT	acid"
XX	MO9920767-Al.
FN	29-APR-1999.
PD	20-OCT-1998; 98WO-US22152.
PF	23-OCT-1997; 97US-0955636.
PR	(MINU ) UNIV MINNESOTA.
XX	Nelaeetuen GL;
PI	WP1; 1999-288309/24.
DR	Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX	acid domain, useful for treating clotting disorders
PT	Claim 11; Page 81; 86pp; English.
PS	This sequence represents a modified GLA (gamma-carboxyglutamic acid)
CC	domain. The invention relates to a vitamin K-dependent polypeptide
CC	comprising a modified GLA domain containing an amino acid substitution
CC	which enhances membrane binding of the modified polypeptide as compared
CC	to the native polypeptide. The polypeptide is used to treat a clotting
CC	disorder by decreasing or increasing clot formation. Modification of the
CC	GLA domain results in a protein which has enhanced membrane binding
CC	affinity as compared to the native protein.

CC		disorder by decreasing or increasing clot formation. Modification of the
CC		GLA domain results in a protein which has enhanced membrane binding
CC		affinity as compared to the native protein.
SQ	Sequence	44 AA;
Query Match	87.4%; Score 166; DB 20; Length 44;	
Best Local Similarity	97.7%; Pred. No. 3,8e-21;	
Matches	43; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
OY	1 ANAFLLXLRGSLRXCKXCQCFXXAXRIFKDXARTLFWISY 44 	
DB	1 ANAFLLXLRGSLRXCKXCQCFXXAXRIFEDAXRTLFWISY 44 	
RESULT 3		
ID	AAV18311 standard; peptide; 44 AA.	
AC	AAV18311;	
DT	17-AUG-1999 (first entry)	
DE	Modified GLA domain of vitamin K-dependent protefn.	
KW	GLA domain; mutcin; vitamin K-dependent protein; clotting disorder; therapy.	
OS	Homo sapiens. Synthetic.	
FH	Key Location/Qualifiers	
FT	Misc-difference 1..44 /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"	
FT		
EN	WO9920767-A1.	
PD	29-APR-1999.	
PF	20-OCT-1998; 98WO-US22152.	
PR	23-OCT-1997; 97US-0955636.	
PA	(MINU ) UNIV MINNESOTA.	
PI	Nelaeetuen GL;	
DR	WPI; 1999-288309/24.	
PT	Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders	
PS	Disclosure; Page 80; 86pp; English.	
CC	This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein.	
SQ	Sequence 44 AA;	
Query Match	86.8%; Score 165; DB 20; Length 44;	
Best Local Similarity	97.7%; Pred. No. 5,6e-21;	
Matches	43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
OY	1 ANAFLLXLRGSLRXCKXCQCFXXAXRIFKDXARTLFWISY 44 	
DB	1 ANAFLLXLRDGSILRXCKXCQCFXXAXRIFKDXARTLFWISY 44 	

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3.6
RESULT 4
AA18305
ID AA18305 standard; peptide, 44 AA.
XX
XX AA18305;
AC
XX 17-AUG-1999 (first entry)
DT
XX
XX Human factor VII GLA domain.
DE
XX GLA domain; vitamin K-dependent protein; clotting disorder;
KW therapy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 1..44
FT /note= "Xaa= gamma-carboxyglutamic acid, or glutamic
FT acid"
XX
XX MO9920767-A1.
XX
XX 29-APR-1999.
XX
XX 20-OCT-1998; 98WO-US22152.
XX
XX 23-OCT-1997; 97US-0955636.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Nelsestuen GL;
XX
XX WPI; 1999-288309/24.
XX
XX Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic
XX acid domain, useful for treating clotting disorders
XX
XX Disclosure; Page 15; 86pp; English.
XX
XX This sequence is the factor VII GLA (gamma-carboxyglutamic acid)
XX domain. The invention relates to a vitamin K-dependent polypeptide
XX comprising a modified GLA domain containing an amino acid substitution
XX which enhances membrane binding of the modified polypeptide as compared
XX to the native polypeptide. The polypeptide is used to treat a clotting
XX disorder by decreasing or increasing clot formation. Modification of the
XX GLA domain results in a protein which has enhanced membrane binding
XX affinity as compared to the native protein.
XX
XX Sequence 44 AA;
SQ
Query Match 86.3%; Score 164; DB 20; Length 44;
Best Local Similarity 97.7%; Pred. No. 8.3e-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 ANAFLLXLRPGSLRXCKXXQCSFXXRXIFKDXRRTGLFWISY 44
Db 1 ANAFLLXLRPGSLRXCKXXQCSFXXRXIFKDXRRTGLFWISY 44
RESULT 5
AAB36395
ID AAB36395 standard; peptide, 44 AA.
XX
XX AAB36395;
AC
XX 27-FEB-2001 (first entry)
DT
XX
XX Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.
DE
XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;
KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;

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KW factor X; prothrombin; enhanced membrane binding affinity;
KW clot formation; thrombolytic; haemostatic; bleeding disorder;
KW thrombosis; clotting disorder; haemophilia A; haemophilia B;
KW liver disease.
XX
XX Homo sapiens.
OS
XX
XX MO20006753-A2.
XX
XX 09-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US11416.
XX
XX 29-APR-1999; 99US-0302239.
XX
XX (MINU ) UNIV MINNESOTA.
XX
XX Nelsestuen GL;
XX
XX WPI; 2001-007226/01.
XX
XX Novel vitamin K-dependent polypeptide useful for treating clotting
XX disorders such as thrombosis and hemophilia, comprises modified
XX gamma-carboxy glutamic acid domain that enhances membrane binding
XX affinity
XX
XX Disclosure; Page 12; 81pp; English.
XX
XX The present invention describes a vitamin K-dependent polypeptide (I)
XX comprising a modified gamma-carboxy glutamic acid (GLA) domain having
XX at least one amino acid substitution, that enhances membrane binding
XX affinity and the activity of the polypeptide relative to a corresponding
XX native vitamin K-dependent polypeptide and inhibits clot formation.
XX (I) can have thrombolytic and haemostatic activities, and can be used
XX as an inhibitor of clot formation. (I) is useful for decreasing clot
XX formation in a mammal, a factor VII or factor IX containing a modified
XX GLA domain is useful for increasing clot formation and for treating a
XX bleeding disorder, including thrombosis and clotting disorders such as
XX haemophilia A, haemophilia B and liver disease. The present sequence
XX represents a wild type human factor VII GLA domain sequence, given in
XX the exemplification of the present invention.
XX
XX Sequence 44 AA;
SQ
Query Match 86.3%; Score 164; DB 22; Length 44;
Best Local Similarity 97.7%; Pred. No. 8.3e-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 ANAFLLXLRPGSLRXCKXXQCSFXXRXIFKDXRRTGLFWISY 44
Db 1 ANAFLLXLRPGSLRXCKXXQCSFXXRXIFKDXRRTGLFWISY 44
RESULT 6
AAB84870
ID AAB84870 standard; Protein; 401 AA.
XX
XX AAB84870;
AC
XX 31-JUL-2001 (first entry)
DT
XX
XX Mutant blood coagulant factor VII (FVII-31).
DE
XX Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;
KW mutant; mutein.
XX
XX Homo sapiens.
OS
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 311..317
FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp
FT -Ser-Pro-Asn substituted by Glu-Ala-Ser-Tyr-Pro-Gly-Lys"

```





FT	Cleavage-site	32..33	/note= "proteolytic site"
FT		35	/note= OTHER
FT	Modified-site		/note= "gamma-carboxyglutamic acid"
FT		38..39	/note= "proteolytic site"
FT	Cleavage-site	42..43	/note= "proteolytic site"
FT		44..45	/note= "proteolytic site"
FT	Cleavage-site	50..61	/note= "proteolytic site"
FT		55..70	/note= OTHER
FT	Modified-site	63	/label= OTHER
FT			/note= "beta-hydroxy-aspartic acid"
FT	Disulfide-bond	72..81	
FT		91..102	
FT	Disulfide-bond	98..112	
FT		114..127	
FT	Disulfide-bond	135..162	
FT		143..144	
FT	Cleavage-site		/note= "proteolytic site"
FT		145	/note= "glycosylation site"
FT	Modified-site		/note= "glycosylation site"
FT		159..164	
FT	Disulfide-bond	178..194	
FT		193	
FT	Active-site	242	
FT		344	
FT	Active-site	290..291	
FT	Cleavage-site		/note= "proteolytic site in unmodified factor VII"
FT		290	/note= "proteolytic site in unmodified factor VII"
FT	Misc-difference		/note= "native Arg290 has been substituted by Ser to provide a proteolytically more stable peptide bond"
FT			
FT	Disulfide-bond	310..329	
FT		315..316	
FT	Cleavage-site		/note= "proteolytic site"
FT		322	
FT	Modified-site		/note= "glycosylation site"
FT		340..368	
FT	Disulfide-bond	341..342	
FT			/note= "proteolytic site"
FT	Cleavage-site	392..393	
FT			/note= "proteolytic site"
FT	Cleavage-site	396..397	
FT			/note= "proteolytic site"
FT	Cleavage-site	402..403	
FT			/note= "proteolytic site"
XX			
XX	US5580560-A.		
XX			
XX	03-DEC-1996.		
XX			
XX	22-AUG-1994;	94US-0293778.	
XX			
XX	09-AUG-1993;	93US-0104509.	
XX	13-NOV-1989;	89US-0434149.	
XX	12-JUN-1992;	92US-0898248.	
XX	12-AUG-1994;	94US-0293778.	
XX			
XX	(NOVO ) NOVO-NORDISK AS.		
XX			
XX	Blorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;		
XX			
XX	WPI; 1997-033523/03.		
XX			
XX	Mutated human factor VII or VIIa proteins - with amino acid		
XX	substitutions to improve proteolytic stability		
XX			
XX	Example 3, Page -; 28pp; English.		

CC Modified human factor VII or VIIa proteins are stabilised against  
 CC proteolytic cleavage by substitution of one of the residues Lys32,  
 CC Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and  
 CC Lys341 by an amino acid that provides a proteolytically more stable  
 CC peptide bond, provided that Lys32 is replaced by Gln, Glu, His,  
 CC Gly, Thr, Ala or Ser. The modified proteins are useful for treating  
 CC bleeding disorders such as thrombocytopenia and von Willebrand's  
 CC disease. They are also suitable for addition to plasma substitutes.  
 CC The present sequence is a specific example of a modified factor VII  
 CC protein.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 CC  
 XX  
 SQ Sequence 406 AA;  
 Query Match 86.3%; Score 164; DB 18; Length 406;  
 Best Local Similarity 75.0%; Pred. No. 8.3e-20;  
 Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
 Oy 1 ANAFLLXLRQGSLLRXCKXXQCSFXXARXIFDAXRTKLFWISY 44  
 Db 1 ANAFLELRPGSLERECKEQCSFEAREIFDAXRTKLFWISY 44  
 RESULT 10  
 AAW14510  
 ID AAW14510 standard; protein; 406 AA.  
 XX  
 AC AAW14510;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 14-MAY-1997 (first entry)  
 XX  
 XX Modified blood coagulation Factor VII (R315S).  
 DE  
 XX  
 KW Blood coagulation; factor 7; mutein; mutation; modification;  
 KM thrombocytopenia; von Willebrand's disease; plasma substitute.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 6 /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT Modified-site 7 /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT Modified-site 14 /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT Modified-site 16 /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT Modified-site 19 /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT Modified-site 20 /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT Disulfide-bond 17..22 /note= "gamma-carboxylutamic acid"  
 FT Modified-site 25 /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT Modified-site 26 /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT Modified-site 29 /label= OTHER  
 FT /note= "gamma-carboxylutamic acid"  
 FT Modified-site 32..33 /note= "gamma-carboxylutamic acid"  
 FT Modified-site 35 /label= OTHER  
 FT /label= OTHER

FT /note= "gamma-carboxylutamic acid"  
 FT Cleavage-site 38..39 /note= "proteolytic site"  
 FT Cleavage-site 42..43 /note= "proteolytic site"  
 FT Cleavage-site 44..45 /note= "proteolytic site"  
 FT Disulfide-bond 50..61 /note= "proteolytic site"  
 FT Disulfide-bond 55..70 /label= OTHER  
 FT Modified-site 63 /note= "beta-hydroxy-aspartic acid"  
 FT Disulfide-bond 72..81 /note= "proteolytic site"  
 FT Disulfide-bond 91..102 /note= "proteolytic site"  
 FT Disulfide-bond 98..112 /note= "proteolytic site"  
 FT Disulfide-bond 114..127 /note= "proteolytic site"  
 FT Disulfide-bond 135..162 /note= "proteolytic site"  
 FT Cleavage-site 143..144 /note= "proteolytic site"  
 FT Modified-site 145 /note= "glycosylation site"  
 FT Disulfide-bond 159..164 /note= "glycosylation site"  
 FT Disulfide-bond 178..194 /note= "glycosylation site"  
 FT Active-site 193 /note= "glycosylation site"  
 FT Active-site 242 /note= "glycosylation site"  
 FT Active-site 344 /note= "glycosylation site"  
 FT Cleavage-site 290..291 /note= "proteolytic site"  
 FT Disulfide-bond 310..329 /note= "proteolytic site"  
 FT Cleavage-site 315..316 /note= "proteolytic site"  
 FT Misc-difference 315 /note= "proteolytic site in unmodified factor VII"  
 FT  
 FT Modified-site 322 /note= "glycosylation site"  
 FT Disulfide-bond 340..368 /note= "glycosylation site"  
 FT Cleavage-site 341..342 /note= "proteolytic site"  
 FT Cleavage-site 392..393 /note= "proteolytic site"  
 FT Cleavage-site 396..397 /note= "proteolytic site"  
 FT Cleavage-site 402..403 /note= "proteolytic site"  
 FT  
 XX US5580560-A.  
 PN  
 XX  
 PD 03-DEC-1996.  
 XX  
 PP 22-AUG-1994; 94US-0293778.  
 XX  
 PR 09-AUG-1993; 93US-0104509.  
 PR 13-NOV-1989; 89US-0434149.  
 PR 12-JUN-1992; 92US-0898248.  
 PR 22-AUG-1994; 94US-0293778.  
 XX  
 PA (NOVO ) NOVO-NORDISK AS.  
 XX  
 PI Bjorn SE, Nicolaisen EM, Wiberg FC, Woodbury R;  
 XX  
 DR WPI; 1997-033523/03.  
 XX  
 PT Mutated human factor VII or VIIa proteins - with amino acid  
 FT substitutions to improve proteolytic stability  
 XX  
 PS Example 4; Page -: 28pp; English.  
 XX  
 CC Modified human factor VII or VIIa proteins are stabilised against  
 CC proteolytic cleavage by substitution of one of the residues Lys32,  
 CC Lys38, Ile42, Tyr44, Phe278, Arg290, Arg304, Arg315, Tyr332 and  
 CC Lys341 by an amino acid that provides a proteolytically more stable

CC peptide bond, provided that Lys32 is replaced by Glu, Glu, His,  
CC Gly, Thr, Ala or Ser. The modified proteins are useful for treating  
CC bleeding disorders such as thrombocytopenia and von Willebrand's  
CC disease. They are also suitable for addition to plasma substitutes.  
CC The present sequence is a specific example of a modified factor VII  
CC protein.  
CC (Updated on 25-MAR-2003 to correct PF field.)

SQ Sequence 406 AA;

Query Match 86.3%; Score 164; DB 18; Length 406;  
Best Local Similarity 75.0%; Pred. No. 8.3e-20;  
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLRXCCKXQCSFYXARXIFKDAKRTKLFWISY 44  
Db 1 ANAFLELRPGSLRBECKECQSFEEAREIKDAERTKLFWISY 44

RESULT 11

AAU77745 ID AAU77745 standard; protein; 406 AA.

AAU77745;

05-JUN-2002 (first entry)

Human factor VIIa active site mutant.

Factor VIIa; human; shock heat treatment; protein stability;  
protein manufacture; protein conformation; mutant; mutain.

Homo sapiens.  
Synthetic.

Location/Qualifiers

Key 193

Active-site /note= "Member of the factor VIIa catalytic triad"

Active-site 242

Active-site /note= "Member of the factor VIIa catalytic triad"

Active-site 344

Misc-difference /note= "Member of the factor VIIa catalytic triad"

FT /label= Gly, Met, Thr

FT /note= "Preferably Ala. Wild type Ser"

W0200177141-A1.

18-OCT-2001.

06-APR-2001; 2001WO-DK0234.

06-APR-2000; 2000DK-0000573.

17-APR-2000; 2000US-197650P.

(NOVO ) NOVO NORDISK AS.

Mathiesen F;

WPI; 2001-657162/75.

Stabilisation of a polypeptide e.g. in a pharmaceutical composition  
involves a shock heat treatment

Disclosure; Page -: 22pp; English.

The invention describes a method of stabilising a polypeptide involving  
shock heat treatment of the polypeptide. The method is useful in a  
pharmaceutical composition, in the industrial or large scale method of  
manufacturing a polypeptide, also as a unit operation during preparation,  
purification, recovery and/or formulation of polypeptides. The shock heat  
treatment improves the protein stability without substantial loss of  
biological activity. The method can be applied to change polypeptide

CC conformation in a very fast and non-invasive manner. The polypeptide  
CC formed is stable. The method is also useful for decreasing the  
CC association of the polypeptide. This sequence represents a modified  
CC human factor VIIa protein, mutated at the catalytic site, described  
CC in the invention.  
CC Note: This sequence does not appear in the specification but has  
CC been obtained using information given in the invention.

SQ Sequence 406 AA;

Query Match 86.3%; Score 164; DB 22; Length 406;  
Best Local Similarity 75.0%; Pred. No. 8.3e-20;  
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ANAFLLXLRGSLRXCCKXQCSFYXARXIFKDAKRTKLFWISY 44  
Db 1 ANAFLELRPGSLRBECKECQSFEEAREIKDAERTKLFWISY 44

RESULT 12

AAM52171 ID AAM52171 standard; Protein; 406 AA.

AAM52171;

07-FEB-2002 (first entry)

Human FVII SEQ ID NO 1.

Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;  
cardiant; hepatotropic; cerebroprotective; haemophilia; liver disease;  
myocardial infarction; thrombotic stroke; deep-vein thrombosis.

Homo sapiens.

Location/Qualifiers

Key 6

Misc-difference /label= Glu, OTHER

Misc-difference /note= "OTHER = gamma carboxylutamic acid"

Misc-difference /label= Glu, OTHER

Misc-difference /note= "OTHER = gamma carboxylutamic acid"

Misc-difference /label= Glu, OTHER

Misc-difference /note= "OTHER = gamma carboxylutamic acid"

Misc-difference /label= Glu, OTHER

Misc-difference /note= "OTHER = gamma carboxylutamic acid"

Misc-difference /label= Glu, OTHER

Misc-difference /note= "OTHER = gamma carboxylutamic acid"

Misc-difference /label= Glu, OTHER

Misc-difference /note= "OTHER = gamma carboxylutamic acid"

Misc-difference /label= Glu, OTHER

Misc-difference /note= "OTHER = gamma carboxylutamic acid"

Misc-difference /label= Glu, OTHER

Misc-difference /note= "OTHER = gamma carboxylutamic acid"

Misc-difference /label= Glu, OTHER

Misc-difference /note= "OTHER = gamma carboxylutamic acid"

Misc-difference /label= Glu, OTHER

Misc-difference /note= "OTHER = gamma carboxylutamic acid"

Misc-difference /label= Glu, OTHER

Misc-difference /note= "OTHER = gamma carboxylutamic acid"

Misc-difference /label= Glu, OTHER

Misc-difference /note= "OTHER = gamma carboxylutamic acid"

Misc-difference /label= Glu, OTHER

Misc-difference /note= "OTHER = gamma carboxylutamic acid"

Misc-difference /label= Glu, OTHER

Misc-difference /note= "OTHER = gamma carboxylutamic acid"

Misc-difference /label= Glu, OTHER

Misc-difference /note= "OTHER = gamma carboxylutamic acid"

Misc-difference /label= Glu, OTHER

Misc-difference /note= "OTHER = gamma carboxylutamic acid"

Misc-difference /label= Glu, OTHER

Misc-difference /note= "OTHER = gamma carboxylutamic acid"

Misc-difference /label= Glu, OTHER

Misc-difference /note= "OTHER = gamma carboxylutamic acid"

```

FT      /note= "proteolytic cleavage site converting FVII zymogen
FT      to an activated form, comprising two chains
FT      linked by a single disulphide bridge"
FT      Modified-site      322
FT      /note= "N-glycosylated"
FN      WO200158935-A2.
XX      16-AUG-2001.
XX      12-FEB-2001; 2001WO-DK00094.
XX      11-FEB-2000; 2000DK-0000218.
XX      18-OCT-2000; 2000DK-0001558.
XX      (MAXY-) MAXYGEN APS.
XX      (MAXY-) MAXYGEN APS.
XX      Andersen KV, Pedersen AH, Bornaes C;
XX      MPI; 2001-581807/65.
XX      N-PSDB; AA199982.
XX      New conjugate, useful for treating Factor VIIa related diseases or
XX      disorders such as haemophilia, liver disease, myocardial infarction and
XX      deep-vein thrombosis, comprises non-polypeptide group covalently
XX      attached to polypeptide group -
XX      Claim 1; Page 81-83; 89pp; English.
XX      The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
XX      polypeptide conjugates, comprising at least one non-polypeptide group
XX      covalently attached to a polypeptide, where the amino acid sequence of
XX      polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
XX      least one amino acid residue containing an attachment group for the
XX      non-polypeptide group has been introduced or removed. The FVIIa
XX      conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
XX      cerebroprotective activity and are useful for treating FVIIa/TF-related
XX      diseases or disorders such as haemophilia, liver disease, myocardial
XX      infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
XX      have increased functional in vivo half life and/or increased plasma half
XX      life, increased bioavailability and/or reduced sensitivity to proteolytic
XX      degradation. Consequently medical treatment using the conjugates has a
XX      number of advantages over currently available such as longer duration
XX      between injections.
XX      Sequence      406 AA;
XX      Query Match      86.3%; Score 164; DB 22; Length 406;
XX      Best Local Similarity 97.7%; Pred. No. 8.3e-20;
XX      Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY      1 ANAFLLXLRQSLXKXCKXKXCFXXARXIFKDXARTLFWISY 44
OY      1 ANAFLLXLRQSLXKXCKXKXCFXXARXIFKDXARTLFWISY 44
DB      1 ANAFLLXLRQSLXKXCKXKXCFXXARXIFKDXARTLFWISY 44

RESULT 13
AAM52172
ID      AAM52172 standard; Protein; 406 AA.
XX      AAM52172;
XX      07-FEB-2002 (first entry)
XX      Mammalian expressed human FVII SEQ ID NO 3.
XX      Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
XX      cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
XX      myocardial infarction; thrombotic stroke; deep-vein thrombosis.
XX      Homo sapiens.
XX      Key      Location/Qualifiers
FH

```

```

FT      Modified-site      52
FT      /note= "O-glycosylated"
FT      Modified-site      60
FT      /note= "O-glycosylated"
FT      Modified-site      145
FT      /note= "N-glycosylated"
FT      Cleavage-site      152..153
FT      /note= "proteolytic cleavage site converting FVII zymogen
FT      to an activated form, comprising two chains
FT      linked by a single disulphide bridge"
FT      Modified-site      322
FT      /note= "N-glycosylated"
FN      WO200158935-A2.
XX      16-AUG-2001.
XX      12-FEB-2001; 2001WO-DK00094.
XX      11-FEB-2000; 2000DK-0000218.
XX      18-OCT-2000; 2000DK-0001558.
XX      (MAXY-) MAXYGEN APS.
XX      Andersen KV, Pedersen AH, Bornaes C;
XX      MPI; 2001-581807/65.
XX      N-PSDB; AA199983.
XX      New conjugate, useful for treating Factor VIIa related diseases or
XX      disorders such as haemophilia, liver disease, myocardial infarction and
XX      deep-vein thrombosis, comprises non-polypeptide group covalently
XX      attached to polypeptide group -
XX      Disclosure; Page 85-86; 89pp; English.
XX      The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
XX      polypeptide conjugates, comprising at least one non-polypeptide group
XX      covalently attached to a polypeptide, where the amino acid sequence of
XX      polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
XX      least one amino acid residue containing an attachment group for the
XX      non-polypeptide group has been introduced or removed. The FVIIa
XX      conjugates have haemostatic, thrombolytic, cardiant, hepatotrophic and
XX      cerebroprotective activity and are useful for treating FVIIa/TF-related
XX      diseases or disorders such as haemophilia, liver disease, myocardial
XX      infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
XX      have increased functional in vivo half life and/or increased plasma half
XX      life, increased bioavailability and/or reduced sensitivity to proteolytic
XX      degradation. Consequently medical treatment using the conjugates has a
XX      number of advantages over currently available such as longer duration
XX      between injections.
XX      Sequence      406 AA;
XX      Query Match      86.3%; Score 164; DB 22; Length 406;
XX      Best Local Similarity 75.0%; Pred. No. 8.3e-20;
XX      Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
OY      1 ANAFLLXLRQSLXKXCKXKXCFXXARXIFKDXARTLFWISY 44
OY      1 ANAFLEELRPGSLERCKEBCSPFEAREIFKDXARTLFWISY 44
DB      1 ANAFLEELRPGSLERCKEBCSPFEAREIFKDXARTLFWISY 44

RESULT 14
AAM52181
ID      AAM52181 standard; Protein; 406 AA.
XX      AAM52181;
XX      07-FEB-2002 (first entry)
XX      Human FVII mutant T106N.
XX

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KW	Factor VII; FVII: Factor VIIa; FVIIa: haemostatic; thrombolytic;
KV	cardiant; hepatotropic; cerebroprotective; haemophilia; liver disease;
KM	myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
KX	mutin.
XX	
OS	Homo sapiens.
XX	Synthetic.
FH	Key
FT	Misc-difference
FT	6 Location/Qualifiers
FT	/label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference
FT	7 /label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference
FT	14 /label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference
FT	16 /label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference
FT	19 /label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference
FT	20 /label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference
FT	25 /label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference
FT	26 /label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference
FT	29 /label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference
FT	35 /label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference
FT	52 /label= Glu, OTHER
FT	/note= "OTHER = gamma carboxyglutamic acid"
FT	Misc-difference
FT	60 /label= Glu, OTHER
FT	/note= "O-glycosylated"
FT	Misc-difference
FT	106 /label= Glu, OTHER
FT	/note= "Wild-type Thr substituted by Asn"
FT	Misc-difference
FT	145 /label= Glu, OTHER
FT	/note= "N-glycosylated"
FT	Cleavage-site
FT	152..153 /note= "proteolytic cleavage site converting FVII zymogen to an activated form, comprising two chains linked by a single disulphide bridge"
FT	Modified-site
FT	322 /note= "N-glycosylated"
FT	
XX	
FN	WO200158935-A2.
XX	
PD	16-AUG-2001.
XX	
PB	12-FEB-2001; 2001WO-DK00094.
XX	
PR	11-FEB-2000; 2000DK-0000218.
PR	18-OCT-2000; 2000DK-0001558.
XX	
PA	(MAXY-) MAXYGEN APS.
XX	
PI	Andersen KV, Pedersen AH, Bornaes C,
XX	
DR	WPI; 2001-581807/65.
XX	
PT	New conjugate, useful for treating Factor VIIa related diseases or
PT	disorders such as haemophilia, liver disease, myocardial infarction and
PT	deep-vein thrombosis, comprises non-polypeptide group covalently
PT	attached to polypeptide group -

XX	Example 3; Page -; 89pp; English.
PS	
CC	The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
CC	polypeptide conjugates, comprising at least one non-polypeptide group
CC	covalently attached to a polypeptide, where the amino acid sequence of
CC	polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
CC	least one amino acid residue containing an attachment group for the
CC	non-polypeptide group has been introduced or removed. The FVIIa
CC	conjugates have haemostatic, thrombolytic, cardiact, hepatotrophic and
CC	cerebroprotective activity and are useful for treating FVIIa/Fr-related
CC	diseases or disorders such as haemophilia, liver disease, myocardial
CC	infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
CC	have increased functional in vivo half life and/or increased plasma half
CC	life, increased bioavailability and/or reduced sensitivity to proteolytic
CC	degradation. Consequently medical treatment using the conjugates has a
CC	number of advantages over currently available such as longer duration
CC	between injections. The present sequence is that of a human FVII mutant,
CC	having an addition in vivo glycosylation site and tested for its
CC	amidolytic activity.
CC	Note: The present sequence is not shown in the specification but is
CC	derived from the human wild-type FVII sequence shown in SEQ ID NO 1
CC	(AAM52171).
CC	
XX	
SQ	Sequence    406 AA;
	Query Match                 86.3%; Score 164; DB 22; Length 406;
	Best Local Similarity      97.7%; Pred. No. 8.3e-20;
	Matches    43; Conservative    0; Mismatches    1; Indels    0; Gaps    0;
OY	
Db	1 ANAFLLXLRQGSLRXCKCXXQCSPXXXXRIFPKAXRTKLFWISY 44   1 ANAFLLXLRPGSLRXCKCXXQCSPFXARXIRFKDAXRTKLFWISY 44
RESULT 15	
AAM52182	
ID	AAM52182 standard; Protein; 406 AA.
AC	
XX	AAM52182;
XX	
DT	07-FEB-2002 (first entry)
XX	
DE	Human FVII mutant K143N/N145T.
XX	
KW	Factor VII; FVII; Factor VIIa; FVIIa; haemostatic; thrombolytic;
KW	cardiant; hepatotrophic; cerebroprotective; haemophilia; liver disease;
KW	myocardial infarction; thrombotic stroke; deep-vein thrombosis; mutant;
KM	muteln.
XX	
OS	Homo sapiens.
OS	
OS	Synthetic.
XX	
TH	Key                          Location/Qualifiers
FT	Misc-difference            6       /label= GIU, OTHER
FT	/note= "OTHER = gamma carboxylutamic acid"
FT	Misc-difference            7       /label= GIU, OTHER
FT	/note= "OTHER = gamma carboxylutamic acid"
FT	Misc-difference            14      /label= GIU, OTHER
FT	/note= "OTHER = gamma carboxylutamic acid"
FT	Misc-difference            16      /label= GIU, OTHER
FT	/note= "OTHER = gamma carboxylutamic acid"
FT	Misc-difference            19      /label= GIU, OTHER
FT	/note= "OTHER = gamma carboxylutamic acid"
FT	Misc-difference            20      /label= GIU, OTHER
FT	/note= "OTHER = gamma carboxylutamic acid"
FT	Misc-difference            25      /label= GIU, OTHER
FT	/note= "OTHER = gamma carboxylutamic acid"

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FT      /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Misc-difference
FT      26 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Misc-difference
FT      29 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Misc-difference
FT      35 /label= Glu, OTHER
FT      /note= "OTHER = gamma carboxyglutamic acid"
FT      Modified-site
FT      52 /note= "O-glycosylated"
FT      Modified-site
FT      60 /note= "O-glycosylated"
FT      Misc-difference
FT      143 /note= "Wild-type Lys substituted by Asn"
FT      Misc-difference
FT      145 /note= "Wild-type Asn substituted by Thr"
FT      Cleavage-site
FT      152..153 /note= "proteolytic cleavage site converting FVII zymogen
FT      to an activated form, comprising two chains
FT      linked by a single disulphide bridge"
FT      Modified-site
FT      322 /note= "N-glycosylated"
FT      WO200158935-A2.
XX      16-AUG-2001.
XX      12-FEB-2001; 2001WO-DK00094.
XX      11-FEB-2000; 2000DK-0000218.
XX      18-OCT-2000; 2000DK-0001558.
XX      (MAXY-) MAXYGEN APS.
XX      Andersen KV, Pedersen AH, Bornaes C;
XX      WPI; 2001-581807/65.
XX      New conjugate, useful for treating Factor VIIa related diseases or
XX      disorders such as haemophilia, liver disease, myocardial infarction and
XX      deep-vein thrombosis, comprises non-polypeptide group covalently
XX      attached to polypeptide group -
XX      Example 3; Page -: 89pp; English.
XX      The invention relates to novel Factor VII (FVII) or Factor VIIa (FVIIa)
XX      polypeptide conjugates, comprising at least one non-polypeptide group
XX      covalently attached to a polypeptide, where the amino acid sequence of
XX      polypeptide differs from that of the wildtype FVIIa (AAM52171) in that at
XX      least one amino acid residue containing an attachment group for the
XX      non-polypeptide group has been introduced or removed. The FVIIa
XX      conjugates have haemostatic, thrombolytic, cardiant, hepatotropic and
XX      cerebroprotective activity and are useful for treating FVIIa/TF-related
XX      diseases or disorders such as haemophilia, liver disease, myocardial
XX      infarction, thrombotic stroke and deep-vein thrombosis. The conjugates
XX      have increased functional in vivo half life and/or increased plasma half
XX      life, increased bioavailability and/or reduced sensitivity to proteolytic
XX      degradation. Consequently medical treatment using the conjugates has a
XX      number of advantages over currently available such as longer duration
XX      between injections. The present sequence is that of a human FVII mutant,
XX      having an addition in vivo glycosylation site and tested for its
XX      amidolytic activity.
XX      Note: The present sequence is not shown in the specification but is
XX      derived from the human wild-type FVII sequence shown in SEQ ID NO 1
XX      (AAM52171).
XX      S quence 406 AA;
XX
XX      Query Match 86.3%; Score 164; DB 22; Length 406;
XX      Best Local Similarity 97.7%; Pred. No. 8.3e-20;

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```

Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy      1 ANAFLXXLRGSLRXCKXGCSFFXAXRIFKDAKRTKLFWISY 44
Db      1 ANAFLXXLRPSSLRXCKXGCSFFXAXRIFKDAKRTKLFWISY 44

```

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Search completed: July 28, 2003, 12:23:52
Job time : 37 sec

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 28, 2003, 12:25:31 ; Search time 32.5 Seconds  
(without alignments)  
160.782 Million cell updates/sec

Title: SEQ3  
Perfect score: 190  
Sequence: 1 ANAFLLXLRGSLRXCKXKX.....XXARXIFKDXRTKLFWISY 44

Scoring table: BLOSUM62  
Gap 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubppaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pep:\*  
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9: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubppaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubppaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubppaa/US09\_NEW\_PUB.pep:\*  
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14: /cgn2\_6/ptodata/2/pubppaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubppaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164	86.3	44	US-10-298-330-3	Sequence 3, Appl1
2	164	86.3	406	US-09-782-587B-1	Sequence 1, Appl1
3	164	86.3	406	US-09-782-587B-3	Sequence 3, Appl1
4	164	86.3	406	US-10-109-498-1	Sequence 1, Appl1
5	164	86.3	406	US-10-255-032-1	Sequence 1, Appl1
6	164	86.3	406	US-10-281-727-1	Sequence 1, Appl1
7	164	86.3	466	US-10-017-122-2	Sequence 2, Appl1
8	144	75.8	40	US-10-298-330-23	Sequence 23, Appl1
9	138	72.6	40	US-10-298-330-22	Sequence 22, Appl1
10	138	72.6	40	US-10-298-330-25	Sequence 25, Appl1
11	137	72.1	40	US-10-298-330-26	Sequence 26, Appl1
12	132	69.5	40	US-10-298-330-24	Sequence 24, Appl1
13	123	64.7	44	US-10-298-330-4	Sequence 4, Appl1
14	114.5	60.3	41	US-10-298-330-27	Sequence 27, Appl1
15	107	56.3	44	US-10-298-330-18	Sequence 18, Appl1

16	102	53.7	419	US-10-182-263-6	Sequence 6, Appl1
17	97	51.1	419	US-10-182-263-3	Sequence 3, Appl1
18	97	51.1	419	US-10-182-263-4	Sequence 4, Appl1
19	97	51.1	419	US-10-182-263-5	Sequence 5, Appl1
20	96	50.5	44	US-10-298-330-2	Sequence 2, Appl1
21	95	50.0	426	US-09-951-121A-1	Sequence 1, Appl1
22	95	50.0	426	US-10-295-682-1	Sequence 1, Appl1
23	88	46.3	45	US-10-298-330-5	Sequence 5, Appl1
24	88	46.3	415	US-09-118-748-2	Sequence 2, Appl1
25	88	46.3	461	US-09-684-901-3	Sequence 3, Appl1
26	88	46.3	461	US-10-132-829-5	Sequence 5, Appl1
27	88	46.3	461	US-10-234-406-6	Sequence 6, Appl1
28	88	46.3	461	US-10-234-406-8	Sequence 8, Appl1
29	86	45.3	44	US-10-298-330-1	Sequence 1, Appl1
30	86	45.3	419	US-09-978-917A-4	Sequence 4, Appl1
31	86	45.3	419	US-10-182-263-1	Sequence 1, Appl1
32	86	45.3	461	US-09-978-917A-2	Sequence 2, Appl1
33	86	45.3	461	US-10-182-263-2	Sequence 2, Appl1
34	85	44.7	622	US-10-020-141-8	Sequence 8, Appl1
35	85	44.7	622	US-10-017-631-2	Sequence 2, Appl1
36	85	44.7	622	US-10-214-932-116	Sequence 116, App
37	85	44.7	622	US-10-172-712-29	Sequence 29, Appl1
38	77.5	40.8	46	US-10-298-330-6	Sequence 6, Appl1
39	74.5	39.2	96	US-09-759-130B-313	Sequence 313, App
40	74.5	39.2	15	US-10-189-123-43	Sequence 43, Appl1
41	74.5	39.2	209	US-09-759-130B-312	Sequence 312, App
42	74.5	39.2	209	US-10-189-123-42	Sequence 42, Appl1
43	74.5	39.2	226	US-09-759-130B-310	Sequence 310, Appl1
44	74.5	39.2	226	US-10-189-123-40	Sequence 40, Appl1
45	67	35.3	44	US-10-298-330-19	Sequence 19, Appl1

## ALIGNMENTS

RESULT 1  
US-10-298-330-3  
: Publication 3, Application US/10298330  
: Publication No. US20030100506A1  
: GENERAL INFORMATION:  
: APPLICANT: Neisestuen, Gary L.  
: TITLE OF INVENTION: Modified Vitamin K-Dependent  
: FILE REFERENCE: 09531-127001  
: CURRENT APPLICATION NUMBER: US/10/298,330  
: CURRENT FILING DATE: 2002-11-18  
: PRIOR APPLICATION NUMBER: 09/497,591  
: PRIOR FILING DATE: 2000-02-03  
: PRIOR APPLICATION NUMBER: 09/302,239  
: PRIOR FILING DATE: 1999-04-29  
: PRIOR APPLICATION NUMBER: 08/955,636  
: PRIOR FILING DATE: 1997-10-23  
: NUMBER OF SEQ ID NOS: 27  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 3  
: LENGTH: 44  
: TYPE: PRT  
: ORGANISM: Homo sapiens  
: FEATURES:  
: NAME/KEY: VARIANT  
: LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 35  
: OTHER INFORMATION: Xaa = gamma carboxyglutamic acid or glutamic acid  
US-10-298-330-3

Query Match 86.3%; Score 164; DB 15; Length 44;  
Best Local Similarity 97.7%; Pred. No. 1.1e-21;  
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLLXLRGSLRXCKXKXQCSFXXARXIFKDXRTKLFWISY 44  
DB 1 ANAFLLXLRGSLRXCKXKXQCSFXXARXIFKDXRTKLFWISY 44

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RESULT 2
US-09-782-587B-1
; Sequence 1, Application US/09782587B
; Publication No. US20030096338A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (6)..(7)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD RES
; LOCATION: (14)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD RES
; LOCATION: (16)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD RES
; LOCATION: (19)..(20)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD RES
; LOCATION: (25)..(26)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD RES
; LOCATION: (29)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
; NAME/KEY: MOD RES
; LOCATION: (35)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
US-09-782-587B-1

Query Match      86.3%; Score 164; DB 11; Length 406;
Best Local Similarity 97.7%; Pred. No. 1e-20;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLXXLRQGSIXRXCXXQCSFXAXRIFKDXARTLFWISY 44
DB 1 ANAFLXXLRPGSLRXKXCKXXQCSFXAXRIFKDXARTLFWISY 44

RESULT 3
US-09-782-587B-3
; Sequence 3, Application US/09782587B
; Publication No. US20030096338A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: ANDERSON, KIM V.
; APPLICANT: BORNAES, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
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; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-587B-3

Query Match      86.3%; Score 164; DB 11; Length 406;
Best Local Similarity 75.0%; Pred. No. 1e-20;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANAFLXXLRQGSIXRXCXXQCSFXAXRIFKDXARTLFWISY 44
DB 1 ANAFLXELRPGSLRCKECCQCSFEAREIFKDXARTLFWISY 44

RESULT 4
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286,200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(406)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

Query Match      86.3%; Score 164; DB 15; Length 406;
Best Local Similarity 97.7%; Pred. No. 1e-20;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ANAFLXXLRQGSIXRXCXXQCSFXAXRIFKDXARTLFWISY 44
DB 1 ANAFLXXLRPGSLRXKXCKXXQCSFXAXRIFKDXARTLFWISY 44

RESULT 5
US-10-255-032-1
; Sequence 1, Application US/10255032
; Publication No. US20030100075A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030100075A10 No. US20030100075A1dsk A/S
; TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
; FILE REFERENCE: 6357-WO
; CURRENT APPLICATION NUMBER: US/10/255,032
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: DK PA 2001 01413
; PRIOR FILING DATE: 2001-09-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation Factor VII
; FEATURE:
```



NAME/KEY: MISC FEATURE  
LOCATION: (1)..(406)  
OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)  
US-10-255-032-1

Query Match 86.3%; Score 164; DB 15; Length 406;  
Best Local Similarity 97.7%; Pred. No. 1e-20;  
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRQSLRXCKXQCSFXXARXIFKDXRTKLFWISY 44  
Db 1 ANAFLXXLRPGSLRXCKXQCSFXXARXIFKDXRTKLFWISY 44

RESULT 6  
US-10-281-727-1  
Sequence 1, Application US/10281727  
Publication No. US20030130191A1  
GENERAL INFORMATION:  
APPLICANT: Persson, Bgon  
TITLE OF INVENTION: Human Coagulation Factor VII  
FILE REFERENCE: 6410.200-US  
CURRENT FILING DATE: 2002-10-28  
PRIOR APPLICATION NUMBER: PA 2001 01627  
PRIOR FILING DATE: 2001-11-02  
PRIOR APPLICATION NUMBER: 60/335,383  
PRIOR FILING DATE: 2001-11-15  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 406  
TYPE: PRT  
ORGANISM: Homo Sapiens  
FEATURE:  
OTHER INFORMATION: Xaa means 4-carboxyglutamic acid  
US-10-281-727-1

Query Match 86.3%; Score 164; DB 16; Length 406;  
Best Local Similarity 97.7%; Pred. No. 1e-20;  
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRQSLRXCKXQCSFXXARXIFKDXRTKLFWISY 44  
Db 1 ANAFLXXLRPGSLRXCKXQCSFXXARXIFKDXRTKLFWISY 44

RESULT 7  
US-10-017-122-2  
Sequence 2, Application US/10017122  
Publication No. US20030087244A1  
GENERAL INFORMATION:  
APPLICANT: McGarity, Jeanette  
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE  
FILE REFERENCE: WMI-007  
CURRENT FILING DATE: 2001-12-14  
PRIOR APPLICATION NUMBER: 60/327,487  
PRIOR FILING DATE: 2001-10-09  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 466  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-017-122-2

Query Match 86.3%; Score 164; DB 15; Length 466;  
Best Local Similarity 75.0%; Pred. No. 1.2e-20;  
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRQSLRXCKXQCSFXXARXIFKDXRTKLFWISY 44  
Db 61 ANAFLXELRPGLERCKEQCSFEPARXIFKDXRTKLFWISY 104

RESULT 8  
US-10-298-330-23  
Sequence 23, Application US/10298330  
Publication No. US20030100506A1  
GENERAL INFORMATION:  
APPLICANT: Neilsen, Gary L.  
TITLE OF INVENTION: Modified Vitamin K-Dependent  
FILE REFERENCE: 09531-127001  
CURRENT APPLICATION NUMBER: US/10/298,330  
CURRENT FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: 09/497,591  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/302,239  
PRIOR FILING DATE: 1999-04-29  
PRIOR APPLICATION NUMBER: 08/955,636  
PRIOR FILING DATE: 1997-10-23  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 23  
LENGTH: 40  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: MOD RES  
LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 35  
OTHER INFORMATION: Xaa = gamma carboxyglutamic acid  
US-10-298-330-23

Query Match 75.8%; Score 144; DB 15; Length 40;  
Best Local Similarity 100.0%; Pred. No. 3.3e-18;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANAFLXXLRQSLRXCKXQCSFXXARXIFKDXRTKLF 40  
Db 1 ANAFLXXLRQSLRXCKXQCSFXXARXIFKDXRTKLF 40

RESULT 9  
US-10-298-330-22  
Sequence 22, Application US/10298330  
Publication No. US20030100506A1  
GENERAL INFORMATION:  
APPLICANT: Neilsen, Gary L.  
TITLE OF INVENTION: Modified Vitamin K-Dependent  
FILE REFERENCE: 09531-127001  
CURRENT APPLICATION NUMBER: US/10/298,330  
CURRENT FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: 09/497,591  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/302,239  
PRIOR FILING DATE: 1999-04-29  
PRIOR APPLICATION NUMBER: 08/955,636  
PRIOR FILING DATE: 1997-10-23  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 22  
LENGTH: 40  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: MOD RES  
LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 35  
OTHER INFORMATION: Xaa = gamma carboxyglutamic acid  
US-10-298-330-22

Query Match 72.6%; Score 138; DB 15; Length 40;  
Best Local Similarity 97.5%; Pred. No. 3.8e-17;  
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANAFXXLRQSLXRXCKXXCQSFXXAXIIFKDXARTKLF 40  
Db 1 ANAFXXLRQSLXRXCKXXCQSFXXAXIIFKDXARTKLF 40

RESULT 10  
US-10-298-330-25

; Sequence 25, Application US/10298330  
; Publication No. US20030100506A1  
; GENERAL INFORMATION:  
; APPLICANT: Nelsestuen, Gary L.  
; TITLE OF INVENTION: Modified Vitamin K-Dependent  
; FILE REFERENCE: 09531-127001  
; CURRENT APPLICATION NUMBER: US/10/298,330  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/497,591  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/302,239  
; PRIOR FILING DATE: 1999-04-29  
; PRIOR APPLICATION NUMBER: 08/955,636  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 32, 35  
; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid  
US-10-298-330-25

Query Match 72.6%; Score 138; DB 15; Length 40;  
Best Local Similarity 97.5%; Pred. No. 3.8e-17;  
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANAFXXLRQSLXRXCKXXCQSFXXAXIIFKDXARTKLF 40  
Db 1 ANAFXXLRQSLXRXCKXXCQSFXXAXIIFKDXARTKLF 40

RESULT 11  
US-10-298-330-26

; Sequence 26, Application US/10298330  
; Publication No. US20030100506A1  
; GENERAL INFORMATION:  
; APPLICANT: Nelsestuen, Gary L.  
; TITLE OF INVENTION: Modified Vitamin K-Dependent  
; FILE REFERENCE: 09531-127001  
; CURRENT APPLICATION NUMBER: US/10/298,330  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/497,591  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/302,239  
; PRIOR FILING DATE: 1999-04-29  
; PRIOR APPLICATION NUMBER: 08/955,636  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 33, 35

; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid  
US-10-298-330-26

Query Match 72.1%; Score 137; DB 15; Length 40;  
Best Local Similarity 97.5%; Pred. No. 5.7e-17;  
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANAFXXLRQSLXRXCKXXCQSFXXAXIIFKDXARTKLF 40  
Db 1 ANAFXXLRQSLXRXCKXXCQSFXXAXIIFKDXARTKLF 40

RESULT 12  
US-10-298-330-24

; Sequence 24, Application US/10298330  
; Publication No. US20030100506A1  
; GENERAL INFORMATION:  
; APPLICANT: Nelsestuen, Gary L.  
; TITLE OF INVENTION: Modified Vitamin K-Dependent  
; FILE REFERENCE: 09531-127001  
; CURRENT APPLICATION NUMBER: US/10/298,330  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/497,591  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/302,239  
; PRIOR FILING DATE: 1999-04-29  
; PRIOR APPLICATION NUMBER: 08/955,636  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 32, 35  
; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid  
US-10-298-330-24

Query Match 69.5%; Score 132; DB 15; Length 40;  
Best Local Similarity 95.0%; Pred. No. 4.3e-16;  
Matches 38; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ANAFXXLRQSLXRXCKXXCQSFXXAXIIFKDXARTKLF 40  
Db 1 ANAFXXLRQSLXRXCKXXCQSFXXAXIIFKDXARTKLF 40

RESULT 13  
US-10-298-330-4

; Sequence 4, Application US/10298330  
; Publication No. US20030100506A1  
; GENERAL INFORMATION:  
; APPLICANT: Nelsestuen, Gary L.  
; TITLE OF INVENTION: Modified Vitamin K-Dependent  
; FILE REFERENCE: 09531-127001  
; CURRENT APPLICATION NUMBER: US/10/298,330  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/497,591  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/302,239  
; PRIOR FILING DATE: 1999-04-29  
; PRIOR APPLICATION NUMBER: 08/955,636  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 44  
; TYPE: PRT  
; ORGANISM: Bos taurus

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; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 34, 35
; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid or glutamic acid
US-10-298-330-4
```

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Query Match 64.7%; Score 123; DB 15; Length 44;
Best Local Similarity 75.0%; Pred. No. 1.8e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 ANAFLLXLRQGSLLRXCKXXQCSFXXARXIFKDXRRTKLPWISY 44
Db 1 ANAFLLXLRQGSLLRXCKXXQCSFXXARXIFRNXXRTRQFWVSY 44
```

## RESULT 14

```
US-10-298-330-27
; Sequence 27, Application US/10298330
; Publication No. US20030100506A1
; GENERAL INFORMATION:
; APPLICANT: Neissestuen, Gary L.
; TITLE OF INVENTION: Modified vitamin K-Dependent
; FILE REFERENCE: 09531-12701
; CURRENT APPLICATION NUMBER: US/10/298,330
; PRIOR APPLICATION NUMBER: 09/497,591
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/302,239
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 08/955,636
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: 7, 8, 15, 17, 20, 21, 26, 27, 30, 33, 35, 36
; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid
US-10-298-330-27
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```
Query Match 60.3%; Score 114.5; DB 15; Length 41;
Best Local Similarity 90.2%; Pred. No. 5.4e-13;
Matches 37; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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```
QY 1 ANA-FLXXLRQGSLLRXCKXXQCSFXXARXIFKDXRRTKLP 40
Db 1 ANAFLLXLRQGSLLRXCKXXQCSFXXARXIFRNXXRTRQFWVSY 41
```

## RESULT 15

```
US-10-298-330-18
; Sequence 18, Application US/10298330
; Publication No. US20030100506A1
; GENERAL INFORMATION:
; APPLICANT: Neissestuen, Gary L.
; TITLE OF INVENTION: Modified vitamin K-Dependent
; FILE REFERENCE: 09531-12701
; CURRENT APPLICATION NUMBER: US/10/298,330
; PRIOR APPLICATION NUMBER: 09/497,591
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/302,239
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 08/955,636
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
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```
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 32, 35, 39
; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid or glutamic acid
US-10-298-330-18
```

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Query Match 56.3%; Score 107; DB 15; Length 44;
Best Local Similarity 68.2%; Pred. No. 1.2e-11;
Matches 30; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
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```
QY 1 ANAFLLXLRQGSLLRXCKXXQCSFXXARXIFKDXRRTKLPWISY 44
Db 1 ANAFLLXLRQGSLLRXCKXXQCSFXXARXIFRNXXRTRQFWVSY 44
```

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Job time : 33.5 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 28, 2003, 12:22:40 ; Search time 20 Seconds  
(without alignments)  
93.084 Million cell updates/sec

Title: SEQ3  
Perfect score: 190  
Sequence: 1 ANAFLXXLRGSLRXCKKX.....XXARXIFKDXRTKLFWISY 44

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	167	87.9	44	3	US-08-955-636-26 Sequence 26, Appl
2	166	87.4	44	3	US-08-955-636-30 Sequence 30, Appl
3	165	86.8	44	3	US-08-955-636-27 Sequence 27, Appl
4	164	86.3	44	3	US-08-955-636-3 Sequence 3, Appl
5	164	86.3	406	1	US-08-293-778-24 Sequence 24, Appl
6	164	86.3	406	1	US-08-295-411-5 Sequence 5, Appl
7	164	86.3	406	2	US-08-955-471-5 Sequence 5, Appl
8	164	86.3	406	5	PCT-US92-10242-5 Sequence 5, Appl
9	164	86.3	444	1	US-08-475-845-2 Sequence 2, Appl
10	164	86.3	444	2	US-08-327-690-2 Sequence 2, Appl
11	164	86.3	444	2	US-08-660-289-2 Sequence 2, Appl
12	164	86.3	444	2	US-08-537-807-2 Sequence 2, Appl
13	164	86.3	444	2	US-08-871-003-2 Sequence 2, Appl
14	164	86.3	444	3	US-08-464-233-2 Sequence 2, Appl
15	164	86.3	444	3	US-09-189-607-2 Sequence 2, Appl
16	164	86.3	444	3	US-09-378-907-2 Sequence 2, Appl
17	164	86.3	444	5	PCT-US94-05779-2 Sequence 2, Appl
18	164	86.3	466	1	US-07-882-202A-4 Sequence 4, Appl
19	164	86.3	466	1	US-08-021-615A-4 Sequence 4, Appl
20	164	86.3	466	1	US-08-321-777-A-4 Sequence 4, Appl
21	164	86.3	466	3	US-09-009-217-14 Sequence 14, Appl
22	164	86.3	466	3	US-09-009-656-14 Sequence 14, Appl
23	164	86.3	466	5	PCT-US93-04493-4 Sequence 4, Appl
24	164	86.3	44	3	US-08-955-636-29 Sequence 29, Appl
25	158	83.2	44	3	US-08-955-636-28 Sequence 28, Appl
26	149	78.4	41	1	US-08-229-280-4 Sequence 4, Appl
27	123	64.7	44	3	US-08-955-636-4 Sequence 4, Appl

28	113	59.5	139	1	US-08-330-978-2	Sequence 2, Appl
29	113	59.5	139	1	US-08-474-042-2	Sequence 2, Appl
30	113	59.5	139	1	US-08-484-558-2	Sequence 2, Appl
31	113	59.5	139	1	US-08-774-592-2	Sequence 2, Appl
32	113	59.5	437	1	US-08-487-037-2	Sequence 3, Appl
33	113	59.5	437	1	US-08-487-037-3	Sequence 3, Appl
34	113	59.5	488	1	US-08-487-037-1	Sequence 1, Appl
35	107	56.3	44	3	US-08-955-636-18	Sequence 18, Appl
36	107	56.3	487	2	US-08-469-486-53	Sequence 53, Appl
37	107	56.3	487	2	US-08-469-658-53	Sequence 53, Appl
38	107	56.3	492	1	US-08-469-486-2	Sequence 2, Appl
39	107	56.3	492	2	US-08-469-658-2	Sequence 2, Appl
40	104	54.7	448	1	US-08-295-411-3	Sequence 3, Appl
41	104	54.7	448	2	US-08-955-471-3	Sequence 3, Appl
42	104	54.7	448	5	PCT-US92-10068-1	Sequence 1, Appl
43	104	54.7	448	5	PCT-US92-10242-3	Sequence 3, Appl
44	104	54.7	488	4	US-09-367-777-44	Sequence 44, Appl
45	104	54.7	488	4	US-09-367-791A-27	Sequence 27, Appl

#### ALIGNMENTS

```
RESULT 1
US-08-955-636-26
; Sequence 26, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neissestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)..(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-26

Query Match      87.9%; Score 167; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 1.3e-21;
Matches 43; Conservative 1; Mismatches 0; Gaps 0;

Cy      1 ANAFLXXLRGSLRXCKKXQCSFXAXRXIFKDXRTKLFWISY 44
Db      1 ANAFLXXLRGSLRXCKKXQCSFXAXRXIFKDXRTKLFWISY 44

RESULT 2
US-08-955-636-30
; Sequence 30, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Neissestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-30
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Query Match      87.4%; Score 166; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 1.9e-21;
Matches 43; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      1 ANAFLXLRQSLRXCKXQCSFXXARXIFKDAVRTLFWISY 44
Db      1 ANAFLXLRQSLRXCKXQCSFXXARXIFKDAVRTLFWISY 44
```

## RESULT 3

```
US-08-955-636-27
; Sequence 27, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-27
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Query Match      86.8%; Score 165; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 2.8e-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy      1 ANAFLXLRQSLRXCKXQCSFXXARXIFKDAVRTLFWISY 44
Db      1 ANAFLXLRQSLRXCKXQCSFXXARXIFKDAVRTLFWISY 44
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## RESULT 4

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US-08-955-636-3
; Sequence 3, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-3
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Query Match      86.3%; Score 164; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 4.2e-21;
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Oy      1 ANAFLXLRQSLRXCKXQCSFXXARXIFKDAVRTLFWISY 44
Db      1 ANAFLXLRQSLRXCKXQCSFXXARXIFKDAVRTLFWISY 44
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RESULT 5
US-08-293-778-24
; Sequence 24, Application US/08293778
; Patent No. 5580560
```

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; GENERAL INFORMATION:
; APPLICANT: Nicolaissen, Else M.
; APPLICANT: Bjorn, Soren E.
; APPLICANT: Wiberg, Finn C.
; APPLICANT: Woodbury, Richard
; TITLE OF INVENTION: MODIFIED FACTOR VII/VIII
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
; STREET: 405 Lexington Avenue, 62nd Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,778
; FILING DATE:
; CLASSIFICATION: 435
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,509
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; FILING DATE: 25-JUN-1987
; APPLICATION NUMBER: DK 3235/87
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; FILING DATE: 25-JUN-1987
; APPLICATION NUMBER: US 07/434,149
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; FILING DATE: 13-NOV-1989
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK88/00103
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; FILING DATE: 24-JUN-1988
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; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 07/898,248
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; FILING DATE: 12-JUN-1992
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; ATTORNEY/AGENT INFORMATION:
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; NAME: Agis, Cheryl H.
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; REGISTRATION NUMBER: 34,086
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; REFERENCE/DOCKET NUMBER: 3129, 224-US
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; TELECOMMUNICATION INFORMATION:
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```
; TELEPHONE: 212-867-0123
```

```
; TELEFAX: 212-867-0298
```

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; INFORMATION FOR SEQ ID NO: 24:
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; SEQUENCE CHARACTERISTICS:
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; LENGTH: 406 amino acids
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; TYPE: amino acid
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```
; STRANDEDNESS: single
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; TOPOLOGY: linear
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```
; MOLECULE TYPE: protein
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```
US-08-293-778-24
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Query Match      86.3%; Score 164; DB 1; Length 406;
Best Local Similarity 75.0%; Pred. No. 4.3e-20;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
```

```
Oy      1 ANAFLXLRQSLRXCKXQCSFXXARXIFKDAVRTLFWISY 44
Db      1 ANAFLYLRPGSLRYCKYQCSFYVARYIFKDAVRTLFWISY 44
```

```
RESULT 6
US-08-295-411-5
```

```
Sequence 5, Application US/08295411
Patent No. 5679639
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Meesters, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Office of Patent Counsel, The Scripps
ADDRESS: Research Institute
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,411
FILING DATE: 22-AUG-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSPR1263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-295-411-5

Query Match 86.3%; Score 164; DB 1; Length 406;
Best Local Similarity 75.0%; Pred. No. 4.3e-20;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQSLRXCKXQCSFXAXRIFKDXARTKLFWISY 44
Db 1 ANAFLELRPGSLRBECKEQCSFEARERIFKDXARTKLFWISY 44

RESULT 7
US-08-955-471-5
Sequence 5, Application US/08955471
Patent No. 5968751
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Meesters, Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Office of Patent Counsel, The Scripps
ADDRESS: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
```

```
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Office of Patent Counsel, The Scripps
ADDRESS: Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,471
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSPR1263.0C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
US-08-955-471-5

Query Match 86.3%; Score 164; DB 2; Length 406;
Best Local Similarity 75.0%; Pred. No. 4.3e-20;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQSLRXCKXQCSFXAXRIFKDXARTKLFWISY 44
Db 1 ANAFLELRPGSLRBECKEQCSFEARERIFKDXARTKLFWISY 44

RESULT 8
PCT-US92-10242-5
Sequence 5, Application PC/TUS9210242
GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Meesters, Rolf
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Office of Patent Counsel, The Scripps
ADDRESS: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
```

```
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242
FILING DATE: 19921118
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR0472P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Region
LOCATION: 1..152
OTHER INFORMATION: /note= "Factor VII Light Chain"
FEATURE:
NAME/KEY: Region
LOCATION: 153..406
OTHER INFORMATION: /note= "Factor VII Heavy Chain"
PCT-US92-10242-5
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Query Match 86.3%; Score 164; DB 5; Length 406;

Best Local Similarity 75.0%; Pred. No. 4.3e-20; Indels 0; Gaps 0;

Matches 33; Conservative 0; Mismatches 11;

```
Qy 1 ANAFLXLRQSLRXCKXQCSFYXARXIFKDAARTKLFWISY 44
Db 1 ANAFLLELRPGSLRECKEQQCSFEAREIFKDAERTKLFWISY 44
```

```
RESULT 9
US-08-475-845-2
Sequence 2, Application US/08475845
Patent No. 5788965
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.24
CURRENT APPLICATION DATA:
```

```
APPLICATION NUMBER: US/08/475,845
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-475-845-2
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Query Match 86.3%; Score 164; DB 1; Length 444;

Best Local Similarity 75.0%; Pred. No. 4.7e-20; Indels 0; Gaps 0;

Matches 33; Conservative 0; Mismatches 11;

```
Qy 1 ANAFLXLRQSLRXCKXQCSFYXARXIFKDAARTKLFWISY 44
Db 39 ANAFLLELRPGSLRECKEQQCSFEAREIFKDAERTKLFWISY 82
```

```
RESULT 10
US-08-327-690-2
Sequence 2, Application US/08327690
Patent No. 5817788
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
```



FILED DATE: 28-FEB-1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-327-690-2

Query Match 86.3%; Score 164; DB 2; Length 444;  
Best Local Similarity 75.0%; Pred. No. 4.7e-20;  
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGSLRXCKXQCSFXXARXIFKDXRTKLFWISY 44  
DB 39 ANAFLELRPGSLRECKECCSFEEARLIFKDAERTKLFWISY 82

RESULT 11  
US-08-660-289-2  
Sequence 2, Application US/08660289  
Patent No. 5833982  
GENERAL INFORMATION:  
APPLICANT: Berkner, Kathleen L.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hart, Charles E.  
APPLICANT: Hedner, Ulla  
APPLICANT: Bregengaard, Claus  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Stewart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,289  
FILING DATE: 28-FEB-1991  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/475,845  
FILING DATE: 07-JUN-1995  
APPLICATION NUMBER: 08/327,690  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/065,725  
FILING DATE: 21-MAY-1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/662,920  
FILING DATE: 28-FEB-1991  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600

TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-660-289-2

Query Match 86.3%; Score 164; DB 2; Length 444;  
Best Local Similarity 75.0%; Pred. No. 4.7e-20;  
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGSLRXCKXQCSFXXARXIFKDXRTKLFWISY 44  
DB 39 ANAFLELRPGSLRECKECCSFEEARLIFKDAERTKLFWISY 82

RESULT 12  
US-08-537-807-2  
Sequence 2, Application US/08537807  
Patent No. 5861374  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/537,807  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/05779  
FILING DATE: 23-MAY-1994  
APPLICATION NUMBER: US 08/065,725  
FILING DATE: 21-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/662,920  
FILING DATE: 28-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-1PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-537-807-2

Query Match 86.3%; Score 164; DB 2; Length 444;  
Best Local Similarity 75.0%; Pred. No. 4.7e-20;  
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1 ANAFLLXLRGSLRXCKXQCSFXXARXIFKDXRTKLFWISY 44  
DB 39 ANAFLELRPGSLRECKECCSFEEARLIFKDAERTKLFWISY 82

RESULT 13  
US-08-871-003-2  
Sequence 2, Application US/08871003  
Patent No. 5997864  
GENERAL INFORMATION:  
APPLICANT: Hart, Charles E.

```

APPLICANT: Petersen, Lars C.
APPLICANT: Hedner, Ulla
APPLICANT: Rasmussen, Mirella E.
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,003
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 90-07C7
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-871-003-2

Query Match      86.3%; Score 164; DB 2; Length 444;
Best Local Similarity 75.0%; Pred. No. 4.7e-20;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGSLLKRCXKXQCSFXXRXIFKDAKRTKLFWISY 44
Db 39 ANAFLELRPGSLERCKEBCQSFEBAREIFKDAERTKLFWISY 82

RESULT 14
US-08-464-233-2
Sequence 2, Application US/08464233
Patent No. 6039944
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,233
FILING DATE:
```

```

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-233-2

Query Match      86.3%; Score 164; DB 3; Length 444;
Best Local Similarity 75.0%; Pred. No. 4.7e-20;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANAFLLXLRQGSLLKRCXKXQCSFXXRXIFKDAKRTKLFWISY 44
Db 39 ANAFLELRPGSLERCKEBCQSFEBAREIFKDAERTKLFWISY 82

RESULT 15
US-09-189-607-2
Sequence 2, Application US/09189607
Patent No. 6168789
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/189,607
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/660,289
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/327,690
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/662,920
; FILING DATE: 28-FEB-1991
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 13952-8-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-189-607-2

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Query Match      86.3%; Score 164; DB 3; Length 444;
Best Local Similarity 75.0%; Pred. No. 4.7e-20;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

```

```

QY      1 ANAFLLXXLRQSLRXCKXQCSFXAXRIFKDAARTLFWISY 44
          |||||  |||||  |||||  |||||  |||||  |||||
Db      39 ANAFLEELRPGSLERECKEBCQCFEABARBIKDAERTLFWISY 82

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Search completed: July 28, 2003, 12:28:21  
 Job time : 21 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 28, 2003, 12:21:05 ; Search time 25 Seconds  
(without alignments)  
169.257 Million cell updates/sec

Title: SEQ4  
Perfect score: 192  
Sequence: 1 ANGFLXXLRGSLKRCRX.....XXAHXIFRNXXRTQFWVS 44

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 76: \*  
2: PIR1: \*  
3: PIR2: \*  
4: PIR3: \*  
5: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	157	81.8	407	1 KFB07	coagulation factor
2	131	68.2	443	2 I46932	coagulation factor
3	123	64.1	466	1 KFH07	coagulation factor
4	107	55.7	461	1 JX0210	protein C (activat
5	106	55.2	461	1 S18994	protein C (activat
6	97	50.5	456	1 KXBO	protein C (activat
7	96	50.0	482	1 EXRT	coagulation factor
8	96	50.0	488	1 EXHU	coagulation factor
9	95	49.5	492	1 EXBO	coagulation factor
10	93	48.4	461	1 KFHU	coagulation factor
11	91	47.4	461	1 KXHU	protein C (activat
12	89	46.4	416	1 KFB0	coagulation factor
13	87	45.3	475	1 EXCH	coagulation factor
14	84	43.8	452	1 A30351	coagulation factor
15	84	43.8	459	2 J00419	coagulation factor
16	80	41.7	622	1 THBU	thrombin (EC 3.4.2
17	80	41.7	642	2 S53433	plasma protein S p
18	77	40.1	617	2 S10511	thrombin (EC 3.4.2
19	77	40.1	618	2 A35827	thrombin (EC 3.4.2
20	75	39.1	642	2 S53434	plasma protein S p
21	75	39.1	676	1 KXHU	plasma protein S p
22	72	37.5	675	1 KXBOS	plasma protein S p
23	71	37.0	625	1 TBB0	thrombin (EC 3.4.2
24	71	37.0	646	2 S38819	plasma protein S -
25	69	35.9	422	1 KXHU	plasma protein 2 p
26	69	35.9	675	1 KXRT	plasma protein S p
27	65	33.9	396	1 KXBO	plasma protein 2 -
28	64	33.3	678	2 B48089	growth arrest-spec
29	63	32.8	673	2 A48089	growth arrest-spec

30	62	32.3	675	1 KXMS	plasma protein S p
31	61	31.8	674	2 I55476	growth potentiatin
32	52	27.1	605	1 M1WLB	E1 protein - bovin
33	52	27.1	620	1 M1WLB2	E1 protein - bovin
34	51	26.6	413	1 VHWNIH	nucleoprotein - in
35	49.5	25.8	594	1 D84859	probable MAP kinase
36	49.5	25.8	603	2 C96575	probable MAP kinase
37	48.5	25.3	576	2 G96763	probable MAP kinase
38	45	23.4	687	2 T08528	O-antigen biosynth
39	45	23.4	1275	2 T18556	hypothetical prote
40	43	22.4	133	2 G81710	hypothetical prote
41	43	22.4	484	2 S43737	protein kinase SLT
42	43	22.4	1217	2 T21403	hypothetical prote
43	42	21.9	145	2 T42280	hypothetical prote
44	42	21.9	219	2 AE2449	hypothetical prote
45	42	21.9	242	2 AF1844	hypothetical prote

## ALIGNMENTS

## RESULT 1

KFB07 coagulation factor VIIa (EC 3.4.21.21) - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 21-May-1990 #sequence\_revision 23-Mar-1995 #text\_change 16-Jul-1999

C:Accession: A31979; C20274

R:Takeya, H.; Kawabata, S.; Nakagawa, K.; Yamamichi, Y.; Miyata, T.; Iwanaga, S.

J. Biol. Chem. 263, 14868-14877, 1988

A:Title: Bovine factor VII. Its purification and complete amino acid sequence.

A:Reference number: A31979; PMID:89008362; PMID:3049594

A:Accession: A31979

A:Molecule type: protein

A:Residues: 1-407 <IRK>

R:McMullen, B.A.; Fujikawa, K.; Kisiel, W.

Biochem. Biophys. Res. Commun. 115, 8-14, 1983

A:Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co

A:Reference number: A20274; PMID:63308813; PMID:6688526

A:Accession: C20274

A:Molecule type: protein

A:Residues: 58-62, 'X', 64-68 <MCM>

A:Note: the residue designated 'X' was determined to be hydroxyaspartic acid

R:Haese, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga,

J. Biochem. 104, 867-868, 1988

A:Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag

A:Reference number: A44556; PMID:89213999; PMID:3149637

A:Contents: annotation

A:Note: structure and location of covalently bound carbohydrate

C:Function:

A:Description: catalyzes the proteolytic activation of coagulation factor X in the presen

gulation factor IX in the presence of calcium and tissue factor

A:Pathway: blood coagulation extrinsic pathway

C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam

F:1-152/Product: coagulation factor VIIa light chain #status experimental <MAI>

F:1-44/Domain: Gla domain homology (fragment) <GLA>

F:50-81/Domain: EGF homology <EGF>

F:91-127/Domain: EGF homology <EG2>

F:153-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>

F:153-387/Domain: trypsin homology <TRY>

F:6,7,14,16,19,20,25,26,29,34,35/Modified site: gamma-carboxyglutamic acid (Glu) #status

F:52-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-368/

F:63/Binding site: carbohydrate (Ser) (covalent) #status experimental

F:145,203/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:152-153/Cleavage site: Arg-Ile (coagulation factor X) #status experimental

F:193,242,344/Active site: His, Asp, Ser #status predicted

F:290-291/Cleavage site: Arg-Gly (coagulation factor Xa) #status experimental

Query Match 81.8%; Score 157; DB 1; Length 407;

Best Local Similarity 70.5%; Pred. No. 9e-20;

Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Oy      1 ANGFLXXLFGSLRXRCRXXLCSPXXAHXIFRNXXRTRQFWVSY 44
        |||||  |||||  |||||  |||||  |||||  |||||
Db      1 ANGFLLELLPGSLRECRBELCSFEEAHEIFRNEERTQFWVSY 44

```

```

RESULT 2
146932
Coagulation factor VII - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
C:Accession: 146932
R:Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
Thromb. Res. 69, 231-238, 1993
A:Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
A:Reference number: 146932; PMID:93190306; PMID:8383365
A:Accession: 146932
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-443 <BR0>
A:Cross-references: GB:SE6300; NID:g2562294; PID:g2662295
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
E:124-83/Domain: Gla domain homology <GLA>
E:89-120/Domain: EGF homology <EG1>
E:130-166/Domain: EGF homology <EG2>
E:192-425/Domain: trypsin homology <TRY>

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Query Match      98.2%; Score 131; DB 2; Length 443;
Best Local Similarity 52.3%; Pred. No. 3,98-15;
Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Oy
1  ANGFLXLRQSLKRCXKLCSEFXKXHXITRMXXRTROFVSVY 44
Db
40  ANSLFELRLPGSLRCKEKEELCSFEAREVQSTERTKQFWITY 83

RESULT 3
KFHUT
coagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1989 #sequence revision 19-May-1994 #text_change 08-Dec-2000
C:Accession: A28332; A23819; A31186; B31186; S63524
R/O:Harz, P.J.; Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; Murti
Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A:Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-dependent
A:Reference number: A28332; MUID:87260948; PMID:3037537
A:Accession: A28332
A:Molecule type: DNA
A:Residues: 1-466 <OH>
A:Cross-references: GB:J02933; NID:g180333; PIND:AAA51983.1; PID:g180334
R:Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A:Title: Characterization of a cDNA coding for human factor VII.
A:Reference number: A23819; MUID:86205965; PMID:3486420
A:Accession: A23819
A:Molecule type: mRNA
A:Residues: 1-466 <HAG>
A:Cross-references: GB:M13232; NID:g182799; PIND:AAA8040.1; PID:g182801
R:Rithum, L.; Bjørn, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.
Biochemistry 27, 7785-7793, 1988
A:Title: Amino acid sequence and posttranslational modifications of human factor VII-a
A:Reference number: A90539; MUID:89088153; PMID:3264725
A:Accession: A31186
A:Molecule type: Protein
A:Residues: 61-212 <THI>
A:Accession: B31186
A:Molecule type: protein
R:Björn, S.; Foster, D.C.; Thim, L.; Wiberg, F.C.; Christensen, M.; Komiyama, Y.; Pedersen
J. Biol. Chem. 266, 11051-11057, 1991
A:Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations and
A:Reference number: A40529; MUID:91250411; PMID:1904059
A:Contents: annotation; carbohydrate binding sites
A:Persson, E.; Petersen, L.C.

```

Eur. J. Biochem. 224, 293-300, 1995  
 Article: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carboxy  
 A:Reference number: S63524; MUID:96096752; PMID:8529655  
 A:Accession: S63524  
 A:Molecule type: protein  
 A:Residues: 61-65;99-103;105-109;213-217;308-312 <PER>  
 C:Genetics:  
 A:Gene: GDB:F7  
 A:Cross-references: GDB:119897; OMIM:227500  
 A:Map position: 13q34-13q34  
 A:Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the preser  
 coagulation factor IX in the presence of calcium and tissue factor  
 A:Pathway: blood coagulation extrinsic pathway  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylatam  
 F:1-40/Domain: signal sequence #status predicted <SIG>  
 F:21-60/Domain: propeptide #status predicted <PRO>  
 F:45-104/Domain: Gla domain homology <GLA>  
 F:61-112/Product: coagulation factor VIIa light chain #status experimental <MAL>  
 F:110-141/Domain: EGF homology <EG1>  
 F:151-187/Domain: EGF homology <EG2>  
 F:213-466/Product: coagulation factor VIIa heavy chain #status experimental <MA2>  
 F:213-467/Domain: trypsin homology <TRY>  
 F:166-67;74;76;79;80;85;86;89;95/Modified site: gamma-carboxyglutamic acid (Glu) #status e  
 F:177-82;110-121;115-130;132-141;151-162;158-172;174-187;195-322;219-224;238-254;370-389;4  
 F:113;150/Binding site: carboxylate (Ser) (covalent) #status experimental  
 F:205;362/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status absent  
 F:1203;382/Binding site: carbohydrate (asn) (covalent) #status experimental  
 F:212;213/Cleavage site: Arg-116 (coagulation factor XIII) #status experimental  
 F:353;302;404/Active site: His, Asp, Ser #status predicted  
 F:350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted

Query Match	64.1%	Score 123	DB 1	Length 466
Best Local Similarity	52.3%	Pred. No. 1e-13		
Matches 23	Conservative 5	Mismatches 16	Indels 0	Gaps 0

  

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		:	:	:
bb	61	ANAALEELRPGSL	RECKEEOCSFEERAREIFPKDERTKLFMISY	104
		:	:	:
		:	:	:

RESULT 4  
 UX0210  
 protein C (activated) (EC 3.4.21.69) precursor - mouse  
 N/Alternate names: vitamin K-dependent serine proteinase  
 N/Species: Mus musculus (house mouse)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #ext\_change 16-Jun-2000  
 A/Accession: UX0210  
 R/Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.  
 J. Biochem. 111, 491-495, 1992  
 A/Title: Isolation and characterization of a mouse protein C cDNA.  
 A/Reference number: UX0210; MUID:92316897; PMID:1618739  
 A/Accession: UX0210  
 A/Molecule type: mRNA  
 A/Residues: 1-461 <TAD>  
 A/Cross-references: GB:10445; NID:g220385; PIDN:BA01235.1; PID:g220386  
 A/Experimental source: liver  
 C/Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that reg  
 B.  
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutamu  
 F:1-33/Domain: signal sequence #status predicted <Sig>  
 F:27-85/Domain: Gla domain homology <Gla>  
 F:34-41/Domain: propeptide #status predicted <PRO>  
 F:42-196,199-461/Product: protein C #status predicted <PRC>  
 F:42-196/Domain: light chain #status predicted <PL>  
 F:91-130/Domain: EGF homology <EG1>  
 F:139-174/Domain: EGF homology <EG2>  
 F:199-461/Domain: heavy chain #status predicted <PCH>  
 F:199-211/Domain: activation peptide #status predicted <ACT>  
 F:212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>



C.Date: 31-Jan-1995 #sequence\_revision 07-Feb-1997 #ext\_change 08-Dec-2000  
 C.Accession: S49075; J04670; PS0191; PS0190; I62745  
 R.Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.  
 Thromb. Res. 80, 63-73, 1995  
 A.Title: Evidence for competition between vitamin K-dependent clotting factors for intra  
 A.Reference number: A58498; PMID:96093366; PMID:8578533  
 A.Accession: S49075  
 A.Molecule type: mRNA  
 A.Residues: 1-482 <ST1>  
 A.Cross-references: EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G506601  
 A.Note: submitted to the EMBL Data Library, June 1994  
 A.Note: neither the complete nucleic acid sequence nor the complete translation are show  
 R.Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.  
 Gene 169, 269-273, 1996  
 A.Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.  
 A.Reference number: J04670; PMID:96194815; PMID:8647460  
 A.Accession: J04670  
 A.Molecule type: mRNA  
 A.Residues: 1-482 <ST1>  
 A.Cross-references: EMBL:X79807; NID:G506600; PIDN:CAA56202.1; PID:G506601  
 A.Experimental source: Cos-1 cell  
 R.Enyoli, K.; Miyazaki, K.; Kato, H.  
 J. Biochem. 109, 890-898, 1991  
 A.Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat pla  
 A.Reference number: PS0190; PMID:92041742; PMID:1718949  
 A.Accession: PS0191  
 A.Molecule type: Protein  
 A.Residues: 41-58, 'X', 60-65 <ENJ1>  
 A.Accession: PS0190  
 A.Molecule type: Protein  
 A.Residues: 183-186, 'X', 188-207 <ENJ2>  
 R.Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Nihno, Y.  
 Eur. J. Haematol. 52, 162-168, 1994  
 A.Title: Analysis of the partial nucleotide sequences and deduced primary structures of  
 A.Reference number: I6196; PMID:94222160; PMID:8168596  
 A.Accession: I62745  
 A.Structure: preliminary; translated from GB/EMBL/DBJ  
 A.Molecule type: DNA  
 A.Residues: 295-383, 'G', 385-455 <MUR>  
 A.Cross-references: GB:D1215; NID:G415309; PIDN:BA04756.1; PID:G455396  
 C.Function:  
 A.Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
 A.Pathway: blood coagulation  
 C.Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C.Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglut  
 F.1-23/Domain: signal sequence #status predicted <SIG>  
 F.24-40/Domain: propeptide #status predicted <PRO>  
 F.25-84/Domain: Gla domain homology <GLA>  
 F.41-179/Product: coagulation factor X light chain #status predicted <LCH>  
 F.90-121/Domain: EGF homology <EG1>  
 F.129-164/Domain: EGF homology <EG2>  
 F.183-482/Product: coagulation factor X heavy chain #status predicted <CH>  
 F.183-231/Domain: activation peptide #status predicted <AP>  
 F.233-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>  
 F.232-460/Domain: trypsin homology <TRY>  
 F.46/47, 54, 56, 65, 66, 69, 72, 79/Modified site: gamma-carboxylglutamic acid (Glu) #stat  
 F.57-62, 90-101, 95-110, 112-120, 139-140, 136-149, 151-164, 172-340, 238-243, 259-275, 388-402, 41  
 F.103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F.187/Binding site: carboxylate (Thr) (covalent) #status experimental  
 F.208/Binding site: carboxylate (Thr) (covalent) #status predicted  
 F.218/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F.231-232/Cleavage site: Arg-116 (coagulation factor IXa, coagulation factor VIIa) #stat  
 F.274, 330, 417/Active site: Arg, Asp, Ser #status predicted

Query Match 50.0%; Score 96; DB 1; Length 482;  
 Best Local Similarity 36.4%; Pred. No. 6.3e-09;  
 Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXLRQGSIXKXCRXXLCSFXXAXHIFRNXXRTQFWWSY 44  
 Db 41 ANSFEELIKGNLRECYBEICSPFEARREVFDENKTEEFNWKY 84

## RESULT 8

EXHU  
 coagulation factor Xa (EC 3.4.21.6) precursor [validated] - human  
 N.Alternate names: Stuart factor  
 C.Species: Homo sapiens (man)  
 C.Date: 15-Nov-1984 #sequence\_revision 02-May-1994 #ext\_change 08-Dec-2000  
 C.Accession: A24478; J00917; A24483; A25853; A22208; A21284; A20362; S39415; I54051; A00  
 R.Leytus, S.P.; Foster, D.C.; Kurechi, K.; Davie, E.W.  
 Biochemistry 25, 5098-5102, 1986  
 A.Title: Gene for human Factor X: a blood coagulation factor whose gene organization is e  
 A.Reference number: A24478; PMID:87026600; PMID:3768336  
 A.Accession: A24478  
 A.Molecule type: DNA  
 A.Residues: 1-488 <LEY>  
 A.Cross-references: GB:L29433; GB:M14327; NID:G459809; PIDN:AAA52764.1; PID:G182831  
 R.Messler, T.L.; Pittman, D.D.; Long, G.L.; Kautman, R.J.; Church, W.R.  
 Gene 99, 291-294, 1991  
 A>Title: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coag  
 A.Reference number: J00917; PMID:91216473; PMID:1902434  
 A.Accession: J00917  
 A.Molecule type: mRNA  
 A.Residues: 1-488 <MES>  
 A.Cross-references: GB:M57285; NID:G182389; PIDN:AAA52421.1; PID:G182390  
 R.Miso, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.  
 J. Biol. Chem. 267, 7395-7401, 1992  
 A>Title: Liver-specific expression of the gene coding for human factor X, a blood coagul  
 A.Reference number: A24485; PMID:92218390; PMID:1313796  
 A.Accession: A24485  
 A.Molecule type: DNA  
 A.Residues: 1-15 <MLA>  
 A.Experimental source: liver  
 A.Note: sequence extracted from NCBI backbone (NCBI:93780, NCBI:93787)  
 R.Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.  
 Gene 41, 311-314, 1986  
 A>Title: Isolation and characterization of human blood-coagulation factor X cDNA.  
 A.Reference number: A25853; PMID:86221713; PMID:3011603  
 A.Accession: A25853  
 A.Molecule type: mRNA  
 A.Residues: 19-284, 'E', 289-488 <KAU>  
 A.Cross-references: GB:M2613; NID:G180335; PIDN:AAA51984.1; PID:G180336  
 R.Pung, M.R.; Hay, C.W.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 3591-3595, 1985  
 A>Title: Characterization of an almost full-length cDNA coding for human blood coagulat  
 A.Reference number: A22208; PMID:85216545; PMID:2582420  
 A.Accession: A22208  
 A.Molecule type: mRNA  
 A.Residues: 13-441, 'S', 443-488 <FUN>  
 A.Cross-references: GB:K03194; NID:G182840; PIDN:AAA52490.1; PID:G182841  
 R.Leytus, S.P.; Chung, D.W.; Kistiel, W.; Kurechi, K.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 3699-3702, 1984  
 A>Title: Characterization of a cDNA coding for human factor X.  
 A.Reference number: A21284; PMID:84222026; PMID:6587384  
 A.Accession: A21284  
 A.Molecule type: mRNA  
 A.Residues: 13-284, 'E', 289-488 <LE2>  
 A.Cross-references: GB:K01886  
 R.McMullen, B.A.; Fujikawa, K.; Kistiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weinst  
 Biochemistry 22, 2875-2884, 1983  
 A>Title: Complete amino acid sequence of the light chain of human blood coagulation fact  
 A.Reference number: A20362; PMID:83257207; PMID:6871167  
 A.Accession: A20362  
 A.Molecule type: Protein  
 A.Residues: 41-179 <MCM>  
 R.Inoue, K.; Morita, T.  
 Eur. J. Biochem. 218, 153-163, 1993  
 A>Title: Identification of O-linked oligosaccharide chains in the activation peptides of  
 A.Reference number: S39414; PMID:94062825; PMID:8234361  
 A.Accession: S39415  
 A.Molecule type: Protein  
 A.Residues: 183-234 <INO>  
 A.Note: glycosylation sites  
 A>Note: identification and characterization of beta-hydroxyaspartic acid  
 R.Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhusanam, K.; Lyman, G.



Gene 84f 517-519, 1989  
A>Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human  
A/Reference number: 154051; MUID:90128299; PMID:2612918  
A/Accession: 154051  
A/Status: translation not shown; translated from GB/EMBL/DBD  
A/Molecule type: DNA  
A/Residues: 1-23 <RES>  
A/Cross-references: GB:M3297; NID:918360; PID:AAA52636.1; PID:9553330  
J.Padmahanabhan, K.; Padmanabhan, K.P.; Tullinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Bile  
J. Mol. Biol. 232, 947-966, 1993  
A>Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.  
A/Reference number: A49458; MUID:93360277; PMID:8355279  
A/Contents: annotation; X-ray crystallography, 2.2 angstroms  
C/Comment: The two chains held together by one disulfide bond are formed from a single-c  
C/Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or  
C/Genetics:  
A/Genes: GDB:F10  
A/Cross-references: GDB:119990; OMIM:227600  
A/Map position: 13q34-13q34  
A/Intons: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1  
A/Note: deficiency of this factor causes Stuart disease  
C/Function:  
A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
A/Pathway: blood coagulation  
C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-40/Domain: propeptide #status predicted <PRO>  
F:25-84/Domain: Gla domain homology <Gla>  
F:41-119/Domain: coagulation factor X light chain #status experimental <LCH>  
F:90-121/Domain: EGF homology <EGF>  
F:129-164/Domain: EGF homology <EG2>  
F:183-488/Domain: coagulation factor X heavy chain #status experimental <HCH>  
F:235-488/Domain: activation peptide #status experimental <APT>  
F:235-462/Domain: trypsin homology <TRY>  
F:46-47,54,56,59,60,65,66,67,79/Modified site: gamma-carboxylglutamic acid (Glu) #stat  
F:57-62/Disulfide bonds: #status predicted  
F:90-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443/  
F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
F:119,211/Binding site: carboxylate (Thr) (covalent) #status experimental  
F:221,231/Binding site: carboxylate (Asn) (covalent) #status experimental  
F:234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat  
F:216,222,419/Active site: His, Asp, Ser #status experimental

Query Match 50.0%; Score 96; DB 1; Length 488;  
Best Local Similarity 36.4%; Pred. No. 6.4e-09;  
Matches 16; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

1 ANGFLXXLRQSLKRXCRXXLSFXXAHXIRNXXRTROFVNSV 44  
41 ANSFLERMKKHRECEMEETCSYBEAREVEDSDKTNEFWNKY 84

RESULT 9  
EXBO  
coagulation factor Xa (BC 3.4.21.6) precursor - bovine  
N/Alternate names: Stuart factor  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 24-Apr-1984 #sequence revision 17-Mar-1987 #text change 16-Jul-1999  
C/Accession: A22867; A14997; A12030; A34412; S39414; A00925  
R/Fung, M.R.; Campbell, R.M.; MacGillivray, T.A.  
Nucleic Acids Res. 12, 4481-4492, 1984  
A>Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing a  
A/Reference number: A22867; MUID:84247315; PMID:6330671  
A/Accession: A22867  
A/Molecule type: mRNA  
A/Residues: 1-487 <FNU>  
A/Cross-references: GB:X00673; NID:9192; PID:CAA25286.1; PID:9193  
R/Enfield, D.L.; Ericsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.  
Biochemistry 19, 659-667, 1980  
A>Title: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).  
A/Reference number: A14997; MUID:80130563; PMID:6766735

A/Accession: A14997  
A/Molecule type: protein  
A/Residues: 41-102, 'N', 104-180 <BNF>  
R/McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coe  
A/Reference number: A20274; MUID:83308813; PMID:6688526  
A/Contents: annotation; revision to residue 103  
R/Titani, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.  
Proc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975  
A>Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.  
A/Reference number: A12030; MUID:76053069; PMID:1059093  
A/Accession: A12030  
A/Molecule type: protein  
A/Residues: 183-292,294-295, 'GDE', 299-334, 336-348, 'AE', 351-354,356-441, 'GKFG', 446-492 <T  
A/Note: carboxylate binding sites and disulfide bonds were determined  
R/Persson, E.; Selander, M.; Linné, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.  
J. Biol. Chem. 264, 16897-16904, 1989  
A>Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal  
A/Reference number: A34412; MUID:89380326; PMID:2789221  
A/Accession: A34412  
A/Molecule type: protein  
A/Residues: 85-126 <PER>  
A/Note: beta-hydroxyaspartic acid site  
R/Inoue, K.; Morita, T.  
Eur. J. Biochem. 218, 153-163, 1993  
A>Title: Identification of O-linked oligosaccharide chains in the activation peptides of.  
A/Reference number: S39414; MUID:94062825; PMID:823461  
A/Accession: S39414  
A/Molecule type: protein  
A/Residues: 183-196,199-209,216-233 <INO>  
A/Note: carboxylate binding sites  
R/Titani, K.; Hermanson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; De  
Biochemistry 11, 4899-4903, 1972  
A>Title: Bovine factor X-1a (activated Stuart factor). Evidence of homology with mammali  
A/Reference number: A12453; MUID:73053314; PMID:4264286  
A/Contents: annotation; active site  
R/Fujikawa, K.; Titani, K.; Davie, E.W.  
Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975  
A>Title: Activation of bovine factor X (Stuart factor): conversion of factor Xalpha to f  
A/Reference number: A13504; MUID:76053121; PMID:1059122  
A/Contents: annotation; activation  
R/Sjog, T.; Bjork, I.; Holmgren, A.; Stenflo, J.  
J. Biol. Chem. 259, 5705-5710, 1984  
A>Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxylglutamic  
A/Reference number: A38024; MUID:84185716; PMID:6546930  
A/Contents: annotation; calcium binding  
R/Morita, T.; Jackson, C.M.  
J. Biol. Chem. 261, 4008-4014, 1986  
A/Reference number: A38025; MUID:86140210; PMID:3949800  
A/Contents: annotation; sulfate binding  
C/Comment: Factor Xa converts prothrombin to thrombin during blood clotting.  
C/Comment: The two chains are formed from a single-chain precursor by the excision of tw  
C/Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), or  
activation.  
C/Comment: Calcium binds to the gamma-carboxylglutamic acid (Gla) residues and, with stron  
C/Comment: The gamma-carboxylglutamic acid residues arise by a posttranslational, vitamin  
C/Genetics:  
A/Genes: F10  
A/Map position: 13q34  
C/Function:  
A/Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam  
F:1-15/Domain: signal sequence #status predicted <SIG>  
F:16-40/Domain: propeptide #status predicted <PRO>  
F:25-84/Domain: Gla domain homology <Gla>  
F:41-180/Domain: coagulation factor X light chain #status experimental <LCH>  
F:90-121/Domain: EGF homology <EGF>  
F:129-164/Domain: EGF homology <EG2>  
F:183-492/Domain: coagulation factor X heavy chain #status experimental <HCH>  
F:183-233/Domain: activation peptide #status experimental <APT>

F.234-492/Product: coagulation factor Xa heavy chain #status experimental <AHC>  
 F.234-461/Domains: trypsin homology <TRY>  
 F.46/47/54/56/59/60/65/66/69/72/75/79/Modified site: gamma-carboxyglutamic acid (Glu) #  
 F.57-62/90-101/110/112-121/129-140/136-149/151-164/162-174/Disulfide bonds: #status F  
 F.103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental  
 F.200/Binding site: sulfate (Tyr) (covalent) (partial) #status experimental  
 F.208/488/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F.233-234/Cleavage site: Arg-11e (coagulation factor IX, coagulation factor VIIa) #stat  
 F.240-245/260-276/389-403/414-442/Disulfide bonds: #status experimental  
 F.275/321/418/Active site: His, Asp, Ser #status predicted

Query Match 49.5%; Score 95; DB 1; Length 492;  
 Best Local Similarity 38.6%; Pred. No. 9/7e-09;  
 Matches 17; Conservative 7; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANGFLXLRQGLXKCRXXLCSFPXAXHIFNXXRTQFWISY 44  
 Db 41 ANSFLEVKQGLNRECELEACSLSEAREFVDAQTDSEFWSKY 84

RESULT 10  
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 coagulation factor IXa (EC 3.4.21.22) precursor [validated] - human  
 N/AAlternate names: antihemophilic factor B; Christmas factor  
 C/Species: Homo sapiens (man)  
 C/Date: 17-Dec-1982 #sequence revision 30-Jun-1987 #text change 15-Sep-2000  
 A/Cross-references: A00922; A37570; A30511; A32989; A26273; A21337; A37546; A36623; A60486; A20  
 R/Yoshitake, S.; Schach, B.G.; Foster, D.C.; Davie, E.W.; Kurachi, K.  
 Biochemistry 24, 3736-3750, 1985  
 A>Title: Nucleotide sequence of the gene for human factor IX (antihemophilic factor B).  
 A/Reference number: A00922; MUID:8600558; PMID:2994716  
 A/Accession: A00922  
 A/Molecule type: DNA  
 A/Residues: 1-461 <YOS>  
 A/Cross-references: GB:K02402; NID:g182612; PIDN:AA59620.1; PID:g182613  
 R/Amson, D.S.; Choo, K.H.; Rees, D.J.G.; Giamelli, F.; Gould, K.; Huddleston, J.A.; Bro  
 EMBO J. 3, 1053-1060, 1984  
 A>Title: The gene structure of human anti-haemophilic factor IX.  
 A/Reference number: A37570; MUID:84236100; PMID:6329734  
 A/Accession: A37570  
 A/Molecule type: DNA  
 A/Residues: 1-461 <ANS>  
 A/Cross-references: GB:K02048  
 R/Reitma, P.H.; Bertina, R.M.; Ploos van Amstel, J.K.; Riemens, A.; Briet, E.  
 Blood 72, 1074-1076, 1988  
 A>Title: The putative factor IX gene promoter in hemophilia B Leyden.  
 A/Reference number: A30511; MUID:88327116; PMID:3416069  
 A/Accession: A30511  
 A/Molecule type: DNA  
 A/Residues: 8-24 <REI>  
 A/Cross-references: EMBL:X55008; NID:g311288; PIDN:CA838245.2; PID:g4469253  
 R/Koberl, D.D.; Bockema, C.D.K.; Beetzede, J.M.; Sommer, S.S.  
 Am. J. Hum. Genet. 45, 448-457, 1989  
 A>Title: Functionally important regions of the factor IX gene have a low rate of polymor  
 A/Reference number: A32989; MUID:89371752; PMID:2773937  
 A/Accession: A32989  
 A/Status: not compared with conceptual translation  
 A/Molecule type: DNA  
 A/Residues: 30-92 <KOE>  
 R/McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Lundblad, R.L.; Roberts, H.R.; Graham, J.B.; S  
 Proc. Natl. Acad. Sci. U.S.A. 82, 2847-2851, 1985  
 A>Title: Evidence for a prevalent dimorphism in the activation peptide of human coagulat  
 A/Reference number: A22673; MUID:85190593; PMID:3857619  
 A/Accession: A22673  
 A/Molecule type: mRNA  
 A/Residues: 1-193, 'T', 195-461 <MCG>  
 A/Cross-references: GB:M11309; NID:g180552; PIDN:AA52023.1; PID:g180553  
 A/Note: the authors translated the codon ACA for residue 29 as Tyr  
 R/Jave, M.; de la Salle, H.; Schamber, F.; Ballard, A.; Kohli, V.; Findeli, A.; Tolstosh  
 Nucleic Acids Res. 11, 2325-2335, 1983  
 A>Title: Isolation of a human anti-haemophilic factor IX cDNA clone using a unique 52-ba  
 A/Reference number: A21337; MUID:83220788; PMID:6687940

A/Accession: A21337  
 A/Molecule type: mRNA  
 A/Residues: 1-193, 'T', 195-461 <JAY>  
 A/Cross-references: GB:J00137; NID:g182610; PIDN:AA52763.1; PID:g182611  
 R/Jagadeeswaran, P.; Lavelle, D.E.; Kaul, R.; Mohandas, T.; Warren, S.T.  
 Somat. Cell Mol. Genet. 10, 465-473, 1984  
 A>Title: Isolation and characterization of human factor IX cDNA: identification of Tag I  
 A/Reference number: A37546; MUID:84300526; PMID:6089357  
 A/Accession: A37546  
 A/Molecule type: mRNA  
 A/Residues: 38-193, 'T', 195-326 <JAG>  
 A/Cross-references: GB:M35672  
 R/Kurachi, K.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 79, 6461-6464, 1982  
 A>Title: Isolation and characterization of a cDNA coding for human factor IX.  
 A/Reference number: A30623; MUID:83065193; PMID:6959130  
 A/Accession: A30623  
 A/Molecule type: mRNA  
 A/Residues: 1-12, 'S', 14-73, 'P', 75-82, 'K', 84-203, 'P', 205-216, 'G', 218-298, 'A', 299-356, 'A', .  
 A/Cross-references: GB:J00136; NID:g182608; PIDN:AA58726.1; PID:g182609  
 A/Experimental source: liver  
 R/Tharakan, J.; Strickland, D.; Burgess, W.; Drohan, W.N.; Clark, D.B.  
 Vox Sang. 38, 21-29, 1990  
 A>Title: Development of an immunoaffinity process for factor IX purification.  
 A/Reference number: A60486; MUID:90194857; PMID:2316207  
 A/Accession: A60486  
 A/Molecule type: protein  
 A/Residues: 47-52, 'XX', 55-60, 'X', 63, 'XX', 65 <THA>  
 R/McMullen, B.A.; Fujikawa, K.; Kisiel, W.  
 Biochem. Biophys. Res. Commun. 115, 8-14, 1983  
 A>Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coe  
 A/Reference number: A20274; MUID:83308813; PMID:6688526  
 A/Accession: A20274  
 A/Molecule type: protein  
 A/Residues: 105-109, 'X', 111-115 <MGM>  
 R/Balland, A.; Faure, T.; Carvallo, D.; Cordier, P.; Ulrich, P.; Fournet, B.; de la Salle  
 Eur. J. Biochem. 172, 565-572, 1988  
 A>Title: Characterisation of two differently processed forms of human recombinant factor  
 A/Reference number: S02527; MUID:88166735; PMID:3280312  
 A/Accession: S02527  
 A/Molecule type: protein  
 A/Residues: 29-63 <BAL>  
 A/Note: processed forms expressed in recombinant system  
 R/Jallat, S.; Perraud, F.; Dalemans, W.; Ballard, A.; Dietrele, A.; Faure, T.; Meullen, i  
 EMBO J. 9, 3295-3301, 1990  
 A>Title: Characterization of recombinant human Factor IX expressed in transgenic mice an  
 A/Reference number: S12058; MUID:91006024; PMID:2209546  
 A/Accession: S12058  
 A/Molecule type: mRNA; protein  
 A/Residues: 1-68 <JAL>  
 A/Note: processed forms expressed in recombinant system  
 R/Hanford, P.A.; Barton, W.; Mayhew, M.; Willis, A.; Beesley, T.; Brownlee, G.G.; Campbell  
 EMBO J. 9, 475-480, 1990  
 A>Title: The first EGF-like domain from human factor IX contains a high-affinity calcium  
 A/Reference number: S12377; MUID:90151623; PMID:2406139  
 A/Accession: S12377  
 A/Molecule type: protein  
 A/Residues: 92-130 <HAN>  
 A/Note: NMR detection of calcium binding by domain expressed in recombinant system  
 R/de la Salle, C.; Charmanlier, J.L.; Baas, M.U.; Schwartz, A.; Wiesel, M.L.; Grunebaum,  
 Thromb. Haemost. 70, 370-371, 1993  
 A>Title: A deletion located in the 3' non translated part of the factor IX gene responsi  
 A/Reference number: S159612; MUID:94054330; PMID:8226150  
 A/Accession: S159612  
 A/Status: translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 444-461 <RES>  
 A/Cross-references: GB:S66752; NID:g439773; PIDN:AA82858.1; PID:g439774  
 R/Stoffel, E.S.; Koeberl, D.D.; Sarkar, G.; Sommer, S.S.  
 Science 239, 491-494, 1988  
 A>Title: Genomic amplification with transcript sequencing.  
 A/Reference number: S159529; MUID:88127096; PMID:3340835  
 A/Accession: S159529

A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 290-359 <R2>  
 A:Cross-references: GB:M19063; NID:g182622; PIDN:AAA52456.1; PID:g182633  
 R:Agarwala, K.L.; Kanabata, S.; Takao, T.; Murata, H.; Shimonishi, Y.; Nishimura, H.; Iw  
 Biochemistry 33, 5167-5171, 1994  
 A:Title: Activation peptide of human factor IX has oligosaccharides O-glycosidically lin  
 A:Reference number: A54255; MUID:94227047; PMID:8172892  
 A:Accession: A54255  
 A:Molecule type: protein  
 A:Residues: 'D',204,'X',206-211,'D',214,'X',216-221,'D', <AG>  
 A:Note: the residues designated 'X' were determined to be threonine bound to carbohydrate  
 R:Di Sciopio, R.G.; Kurachi, K.; Davie, E.W.  
 J. Clin. Invest. 61, 1528-1538, 1978  
 A:Title: Activation of human factor IX (Christmas factor).  
 A:Reference number: A18483; MUID:78194509; PMID:659613  
 A:Contents: annotation; activation; active site; carbohydrate binding  
 R:McGraw, R.A.; Davis, L.M.; Noyes, C.M.; Graham, J.B.; Roberts, H.R.; Stafford, D.W.  
 Am. Soc. Hematol. Abstr. 64(Suppl.1), 262a, 1984  
 A:Reference number: A37569  
 A:Contents: annotation  
 A:Note: 194-Thr was also found  
 R:Moritz, T.; Isaacs, B.S.; Esmen, C.T.; Johnson, A.E.  
 J. Biol. Chem. 259, 5698-5704, 1984  
 A:Title: Derivatives of blood coagulation factor IX contain a high affinity Ca2+-binding  
 A:Reference number: A37543; MUID:84185715; PMID:6425296  
 A:Contents: annotation; calcium binding  
 R:Moritz, T.; Isaacs, B.S.; Esmen, C.T.; Johnson, A.E.  
 J. Biol. Chem. 260, 2583, 1985  
 A:Reference number: A37544  
 A:Contents: annotation; calcium binding, correction  
 R:Berclay, A.K.; Rees, D.J.G.; Rizza, C.; Brownlee, G.G.  
 Cell 45, 343-348, 1986  
 A:Title: Defective propeptide processing of blood clotting factor IX caused by mutation  
 A:Reference number: A37545; MUID:86189947; PMID:3009023  
 A:Contents: annotation; signal sequence cleavage site  
 R:Stehito, K.; Kawabata, S.I.; Miyata, T.; Takeya, H.; Takamatsu, J.; Ogata, K.; Kamiya,  
 J. Biol. Chem. 264, 21257-21265, 1989  
 A:Title: Blood clotting factor IX B (M) Nagoya: substitution of arginine 180 by tryptophan  
 A:Reference number: A30622; MUID:90078229; PMID:2592373  
 A:Contents: annotation; sequence of mutant B(M) Nagoya  
 R:Baron, M.; Norman, D.G.; Harvey, T.S.; Hanford, P.A.; Mayhew, M.; Tse, A.G.D.; Brownle  
 submitted to the Brookhaven Protein Data Bank, November 1991  
 A:Reference number: A51252; PDB:1IXA  
 A:Contents: annotation; conformation by (1)H-NMR, residues 92-130  
 A:Note: recombinant form expressed in yeast  
 C:Comment: Factor IX is activated by factor XIa, which excises the activation peptide pr  
 C:Comment: The gamma-carboxyglutamic acid residues arise by posttranslational, vitamin K  
 C:Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strc  
 C:Genetics:  
 A:Gene: GDB:F9  
 A:Cross-references: GDB:119900; OMIM:306900  
 A:Map position: Xq27.1-Xq27.2  
 A:Introns: 30/1; 84/2; 93/1; 131/1; 174/1; 241/3; 280/1  
 C:Function:  
 A:Description: catalyzes the proteolytic activation of coagulation factor X in the prese  
 A:Pathway: blood coagulation intrinsic pathway  
 C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutan  
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 F:29-46/Domain: propeptide #status experimental <PPT>  
 F:31-91/Domain: Gla domain homology <GLA>  
 F:47-191/Product: coagulation factor IXa light chain #status experimental <ALC>  
 F:97-128/Domain: EGF homology <EG1>  
 F:134-170/Domain: EGF homology <EG2>  
 F:192-226/Domain: activation peptide #status experimental <ACT>  
 F:227-461/Product: coagulation factor IXa heavy chain #status experimental <AHC>  
 F:227-464/Domain: trypsin homology <TRY>  
 F:53-54,61,63,66,67,72,73,76,79,82,86/Modified site: gamma-carboxyglutamic acid (Glu) #  
 F:64-69,97-108,102-117,119-128,134-141,141-155,157-170,178-335,252-268,382-396,407-435/D  
 F:99/Binding site: carbohydrate (Ser) (covalent) #status experimental  
 F:110/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

F:191-192/Cleavage site: Arg-Ala (coagulation factor XIa) #status experimental  
 F:203,213/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:205,215/Binding site: carbohydrate (Thr) (covalent) #status experimental  
 F:226-227/Cleavage site: Arg-Val (coagulation factor XIa) #status experimental  
 Query Match 48.4%; Score 93; DB 1; Length 461;  
 Best Local Similarity 41.9%; Pred. No. 2.1e-08;  
 Matches 18; Conservative 4; Mismatches 21; Indels 0; Gaps 0;  
 Oy 2 NGFLXLRQSLKRXCKXLCSEFXAXHXRNRXRRQFVSVY 44  
 Db 49 SGKLEFVQNLRECMERKSEAEAREVENTERTEFWKQY 91  
 RESULT 11  
 KKHU  
 protein C (activated) (EC 3.4.21.69) precursor - human  
 N:Alternate names: autoproteolysin IIA; plasma protein C  
 C:Species: Homo sapiens (man)  
 C:Date: 17-Mar-1987 #sequence revision 17-Mar-1987 #text\_change 16-Jul-1999  
 C:Accession: A22331; A25426; A21781; A23789; A00927  
 R:Forster, D.C.; Yoshitake, S.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 4673-4677, 1985  
 A:Title: The nucleotide sequence of the gene for human protein C.  
 A:Reference number: A22331; MUID:85270390; PMID:2991887  
 A:Accession: A22331  
 A:Molecule type: DNA  
 A:Residues: 1-461 <FOS1>  
 A:Cross-references: GB:M1228; NID:g190333; PIDN:AAA60166.1; PID:g190334  
 R:Plutsky, J.; Hoskins, J.A.; Long, G.L.; Crabtree, G.R.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 546-550, 1986  
 A:Title: Evolution and organization of the human protein C gene.  
 A:Reference number: A25426; MUID:86120978; PMID:3511471  
 A:Molecule type: DNA  
 A:Residues: 1-445,'L',446-461 <PLU>  
 A:Cross-references: GB:M12712; NID:g190330; PIDN:AAA60165.1; PID:g190332  
 R:Forster, D.; Davie, E.W.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 4766-4770, 1984  
 A:Title: Characterization of a cDNA coding for human protein C.  
 A:Reference number: A21781; MUID:84272714; PMID:6589623  
 A:Accession: A21781  
 A:Molecule type: mRNA  
 A:Residues: 'O',107-461 <FOS2>  
 A:Cross-references: GB:X02059; NID:g190322; PIDN:AAA60164.1; PID:g190323  
 R:Beckmann, R.U.; Schmitt, R.U.; Santerre, R.F.; Plutsky, J.; Crabtree, G.R.; Long, G.L.  
 Nucleic Acids Res. 13, 5233-5247, 1985  
 A:Title: The structure and evolution of a 461 amino acid human protein C precursor and it  
 A:Reference number: A23789; MUID:85269639; PMID:2991859  
 A:Accession: A23789  
 A:Molecule type: mRNA  
 A:Residues: 1-461 <BEC>  
 A:Cross-references: GB:X02750; NID:g35689; PIDN:CAA26528.1; PID:g763120  
 R:Malterich, J.P.; Broze Jr., G.J.  
 J. Biol. Chem. 265, 11397-11404, 1990  
 A:Title: Beta protein C is not glycosylated at asparagine 329. The rate of translation me  
 A:Reference number: A44605; MUID:90293094; PMID:164179  
 A:Contents: annotation; carbohydrate binding sites; activation peptide  
 A:Note: the alpha form of protein C is glycosylated at Asn-329, and the beta form is not  
 R:Harrit, R.U.; Ling, V.T.; Spellman, M.W.  
 J. Biol. Chem. 267, 5102-5107, 1992  
 A:Title: O-linked fucose is present in the first epidermal growth factor domain of factor  
 A:Reference number: A44606; MUID:92184750; PMID:1544884  
 A:Contents: annotation; beta-hydroxyaspartic acid  
 C:Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that in  
 C:Comment: Protein C is strongly enhanced by complexing with protein S. Protein C also fe  
 C:Comment: Protein C is synthesized in the liver as a single chain precursor, which is c  
 C:Comment: Protein C is synthesized from the amino end of the heavy chain; this reaction,  
 C:Genetics:  
 A:Gene: GDB:PROC  
 A:Cross-references: GDB:120317; OMIM:176860  
 A:Map position: 2q13-2q21  
 A:Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1



Matches 16; Conservative 7; Mismatches 21; Indels 0; Gaps 0;  
Qy 1 ANGFLXXLRQSLKRCXKXLCFFXXAHXIFRNXXRTROFWVSX 44  
Db 41 ANSLFEMKQCNIRRECEERKCSFEARAEAFEDNEKTEEFWKQY 84

## RESULT 14

coagulation factor IXa (EC 3.4.21.22) precursor - dog  
A:Species: Canis lupus familiaris (dog)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: A30351; I46201  
R:Evans, J.P.; Matzke, H.H.; Ware, J.L.; Stafford, D.W.; High, K.A.  
BioRxiv 74, 207-212, 1989  
A:Title: Molecular cloning of a cDNA encoding canine factor IX.  
A:Reference number: A30351; PMID:8932338; PMID:2752110  
A:Accession: A30351  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-452 <EVA>  
A:Cross-references: GB:M21757; NID:g972719; PIDN:AAA75006.1; PID:g163948  
R:Abelrod, J.H.; Read, M.S.; Brinkhaus, K.M.; Verma, I.M.  
Proc. Natl. Acad. Sci. U.S.A. 87, 5173-5177, 1990  
A:Title: Phenotypic correction of factor IX deficiency in skin fibroblasts of hemophilic  
A:Reference number: I46201; PMID:90311364; PMID:2367529  
A:Accession: I46201  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-452 <AAE>  
A:Cross-references: GB:M33826; NID:g163949; PIDN:AAA30844.1; PID:g163950  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylatan  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-40/Domain: propeptide #status predicted <PRO>  
F:24-84/Domain: Gla domain homology <GLA>  
F:41-452/Product: coagulation factor IX #status predicted <MAT>  
F:90-121/Domain: EGF homology <EG1>  
F:127-163/Domain: EGF homology <EG2>  
F:218-445/Domain: trypsin homology <TRY>  
F:46,47,54,56,59,60,65,66,69,75,79/Modified site: gamma-carboxylglutamic acid (Glu) #  
F:57-62,90-101,95-110,112-121,127-138,134-148,150-163,171-326,243-259,373-387,398-426/Dist  
F:258,306,402/Active site: His, Asp, Ser #status predicted

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Best Local Similarity 37.2%; Pred. No. 7.9e-07;  
Matches 16; Conservative 6; Mismatches 21; Indels 0; Gaps 0;  
Qy 2 NGFLXXLRQSLKRCXKXLCFFXXAHXIFRNXXRTROFWVSX 44  
Db 42 SGKLEFVRGNLRECEERKCSFEARAEAFEDNEKTEEFWKQY 84

## RESULT 15

coagulation factor IXa (EC 3.4.21.22) precursor - mouse (fragment)  
A:Species: Mus musculus (house mouse)  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 16-Jul-1999  
C:Accession: J00419; I49667  
R:Wu, S.M.; Stafford, D.W.; Ware, J.  
Gene 86, 275-278, 1990  
A:Title: Deduced amino acid sequence of mouse blood-coagulation factor IX.  
A:Reference number: J00419; PMID:90215309; PMID:2323576  
A:Accession: J00419  
A:Molecule type: mRNA  
A:Residues: 1-459 <WDS>  
A:Cross-references: GB:M23109; NID:g193317; PIDN:AAA37629.1; PID:g387158  
A:Experimental source: liver  
R:Sarkar, G.; Koeberl, D.D.; Sommer, S.S.  
Genomics 6, 133-143, 1990  
A:Title: Direct sequencing of the activation peptide and the catalytic domain of the fac  
A:Reference number: I46580; PMID:90152675; PMID:2303254  
A:Accession: I49667

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 168-362, 'Q', 364-387, 'I', 389-451 <RSE>  
A:Cross-references: GB:M26236; NID:g193319; PIDN:AAA37630.1; PID:g193320  
C:Comment: This protein plays a critical role in blood coagulation.  
C:Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
C:Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylglutam  
F:1-16/Domain: signal sequence (fragment) #status predicted <SIG>  
F:17-34/Domain: propeptide #status predicted <PRO>  
F:19-79/Domain: Gla domain homology <GLA>  
F:35-459/Product: coagulation factor IX #status predicted <MAT>  
F:85-116/Domain: EGF homology <EG1>  
F:122-158/Domain: EGF homology <EG2>  
F:225-452/Domain: trypsin homology <TRY>  
F:41,42,49,51,54,55,60,61,64,67,70,74/Modified site: gamma-carboxylglutamic acid (Glu) #  
F:52-57,85-96,90-105,107-116,122-133,129-143,145-158,166-333,250-286,380-394,405-433/Dist  
F:265,313,409/Active site: His, Asp, Ser #status predicted

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Best Local Similarity 37.2%; Pred. No. 8e-07;  
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Qy 2 NGFLXXLRQSLKRCXKXLCFFXXAHXIFRNXXRTROFWVSX 44  
Db 37 SGKLEFVRGNLRECEERKCSFEARAEAFEDNEKTEEFWKQY 79

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Job time : 26 secs

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OM protein - protein search, using sw model

Run on: July 28, 2003, 12:12:00 ; Search time 13.5 Seconds

(without alignments)  
153.272 Million cell updates/sec

Title: SEQ4  
Perfect score: 192  
Sequence: 1 ANGFLXXLRGSLXKRCRX.....XXAHXIFRNXXRTQFWVSY 44

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	157	81.8	407	FA7_BOVIN	P22457 bos taurus
2	131	68.2	444	FA7_RABIT	P98139 oryctolagus
3	123	64.1	466	FA7_HUMAN	P08709 homo sapien
4	113	58.9	218	TWGI_HUMAN	O14668 homo sapien
5	107	55.7	461	PRTC_MOUSE	P33587 mus musculu
6	106	55.2	446	FA7_MOUSE	P70375 mus musculu
7	106	55.2	461	PRTC_RAT	P31394 rattus norv
8	105	54.7	231	TWGI_HUMAN	O99122 sus scrofa
9	102	53.1	459	PRTC_PIG	O99122 sus scrofa
10	97	50.5	456	PRTC_BOVIN	P00742 bos taurus
11	96	50.0	488	FA10_HUMAN	P00743 bos taurus
12	95	49.5	492	FA10_BOVIN	P00743 bos taurus
13	94	49.0	490	FA10_RABIT	O19045 oryctolagus
14	93	48.4	461	FA9_HUMAN	P00740 homo sapien
15	91	47.4	461	PRTC_HUMAN	P04070 homo sapien
16	89	46.4	456	FA9_BOVIN	P00741 bos taurus
17	87	45.3	475	FA10_CHICK	P23155 gallus gall
18	84	43.8	452	FA9_CANFA	P19540 canis faml
19	84	43.8	458	PRTC_RABIT	O26661 oryctolagus
20	84	43.8	459	FA9_MOUSE	P12994 mus musculu
21	80	41.7	622	THRB_HUMAN	P00734 homo sapien
22	77	40.1	617	THRB_RAT	P18292 rattus norv
23	77	40.1	618	THRB_MOUSE	P18221 mus musculu
24	75	39.1	649	PRTS_MACU	O28520 macaca mula
25	75	39.1	676	PRTS_HUMAN	P07225 homo sapien
26	72	37.5	675	PRTS_BOVIN	P07224 bos taurus
27	71	37.0	625	THRB_HUMAN	O14669 homo sapien
28	71	37.0	625	THRB_BOVIN	P00735 bos taurus
29	71	37.0	646	PRTS_RABIT	P98118 oryctolagus
30	70	36.5	226	TWGI_HUMAN	O99246 homo sapien
31	69	35.9	376	FA10_TROCA	P81428 tropidichis
32	69	35.9	400	PRTZ_HUMAN	P22891 homo sapien
33	69	35.9	675	PRTS_RAT	P53813 rattus norv

34	65	33.9	396	1	PRTZ_BOVIN	P00744 bos taurus
35	62	32.3	675	1	PRTS_MOUSE	O08761 mus musculu
36	52	27.1	604	1	VE1_BPV2	P11298 bovine papl
37	52	27.1	605	1	VE1_BPV1	P03116 bovine papl
38	51	26.6	433	1	NCAP_INNV	P16691 infectious
39	47.5	24.7	184	1	ADML_MOUSE	P97297 mus musculu
40	45	23.4	1275	1	RFBC_MYXXA	O50864 myxococcus
41	44	22.9	2812	1	ZAN_HUMAN	O39493 homo sapien
42	43	22.4	484	1	SLT2_YEAST	O00772 saccharomyc
43	42	21.9	320	1	GSHB_BUCAI	P57612 buchnera ap
44	42	21.9	345	1	VG59_HSV1	O00138 ictatuid h
45	41	21.4	529	1	VGLP_MEAST	P26031 measles vir

## ALIGNMENTS

RESULT 1  
FA7\_BOVIN ID - FA7\_BOVIN STANDARD; PRT; 407 AA.  
AC P22457;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion accelerator).  
GN F7.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_Taxid=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=89008362; PubMed=3049594;  
RA Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,  
RA Iwanaga S.;  
RT "Bovine factor VII. Its purification and complete amino acid  
RT sequence.";  
RL J. Biol. Chem. 263:14868-14877(1988).  
RN [2]  
RP STRUCTURE OF CARBOHYDRATE ON SER-52.  
RX MEDLINE=9213999; PubMed=1149637;  
RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,  
RA Miyata T., Iwanaga S., Takao T., Shimomishi Y., Ikenaka T.;  
RT "A new trisaccharide sugar chain linked to a serine residue in bovine  
RT blood coagulation factors VII and IX.";  
RL J. Biochem. 104:867-868(1988).  
RN [3]  
RP STRUCTURE OF CARBOHYDRATE ON SER-52.  
RX MEDLINE=91344709; PubMed=2129367;  
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.;  
RT "A new trisaccharide sugar chain linked to a serine residue in the  
RT first EGF-like domain of clotting factors VII and IX and protein Z.";  
RL Adv. Exp. Med. Biol. 281:121-131(1990).  
RN [4]  
RP FUNCTION. CIRCULATES IN THE BLOOD IN A ZWOGEN FORM. FACTOR VII IS  
RP CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR  
RP THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR  
RP AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa  
RP BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO  
RP FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM.  
RN [5]  
RP CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to  
RP form factor Xa.  
RN [6]  
RP SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED  
RP BY A DISULFIDE BOND.  
RN [7]  
RP TISSUE SPECIFICITY: Plasma.  
RN [8]  
RP -1- PM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
RP GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
RP CALCIUM.  
RN [9]  
RP -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
RN [10]  
RP -1- SIMILARITY: Contains 2 EGF-like domains.  
DR PIR; A31979; KFB07.  
DR HSSP; P08709; 1BF9.

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DR MEROPS; S01.215; -.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_T1.
DR InterPro; IPR006209; EGF_T1.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFbLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
KW EGF-like domain; Repeat.
FT CHAIN 1 152 FACTOR VII LIGHT CHAIN.
FT CHAIN 153 407 FACTOR VII HEAVY CHAIN.
FT DOMAIN 6 35 GLA-RICH.
FT DOMAIN 46 82 EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 87 128 EGF-LIKE 2.
FT DOMAIN 153 407 SERINE PROTEASE.
FT SITE 152 153 CLEAVAGE (BY FACTOR XA, FACTOR XIIA,
ACT SITE 193 193 FACTOR IXA, OR THROMBIN).
ACT SITE 242 242 BY SIMILARITY.
ACT SITE 344 344 BY SIMILARITY.
BINDING 338 338 SUBSTRATE (BY SIMILARITY).
DISULFID 17 22 BY SIMILARITY.
DISULFID 50 61 BY SIMILARITY.
DISULFID 55 70 BY SIMILARITY.
DISULFID 72 81 BY SIMILARITY.
DISULFID 91 102 BY SIMILARITY.
DISULFID 98 112 BY SIMILARITY.
DISULFID 114 127 BY SIMILARITY.
DISULFID 135 262 BY SIMILARITY.
DISULFID 159 164 BY SIMILARITY.
DISULFID 178 194 BY SIMILARITY.
DISULFID 310 329 BY SIMILARITY.
DISULFID 340 368 BY SIMILARITY.
MOD_RES 6 6 GAMMA-CARBOXYGLUTAMIC ACID.
MOD_RES 7 7 GAMMA-CARBOXYGLUTAMIC ACID.
MOD_RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID.
MOD_RES 16 16 GAMMA-CARBOXYGLUTAMIC ACID.
MOD_RES 19 19 GAMMA-CARBOXYGLUTAMIC ACID.
MOD_RES 20 20 GAMMA-CARBOXYGLUTAMIC ACID.
MOD_RES 25 25 GAMMA-CARBOXYGLUTAMIC ACID.
MOD_RES 26 26 GAMMA-CARBOXYGLUTAMIC ACID.
MOD_RES 29 29 GAMMA-CARBOXYGLUTAMIC ACID.
MOD_RES 35 35 GAMMA-CARBOXYGLUTAMIC ACID.
MOD_RES 52 52 O-LINKED (GLC. . .).
CARBOHYD 145 145 N-LINKED (GLCNAC. . .).
CARBOHYD 203 203 N-LINKED (GLCNAC. . .).
SEQUENCE 407 AA; 44431 MW; 703E1FE0636F7E10 CRC64;
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Query Maxch 81.8%; Score 157; DB 1; Length 407;
Best Local Similarity 70.5%; Pred. No. 5.2e-21;
Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
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Qy 1 ANGFLXKIRGSLXKRCXKXKCSFXKXKXKIRNXXRTROFVNSY 44
Db 1 ANGFLXELLPQSLERECREELCSFEAHKIFRNEERTROFVNSY 44

RESULT 2
FA7_RABIT STANDARD; PRT; 444 AA.
ID FA7_RABIT P98139; P79224;
AC 01-FEB-1996 (Rel. 33, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
DE F7.
GN Oryctolagus cuniculus (Rabbit).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
OX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=93190306; PubMed=8383365;
RX Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A.;
RT "Complete nucleotide sequence of the cDNA encoding rabbit coagulation
RT factor VII."
RT Thromb. Res. Suppl. 69:231-238 (1993).
RN [2]
RP REVISION TO 395.
RC TISSUE=Liver;
RA Ruiz S.R., Blajchman M.A., Clarke B.J.;
RA Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZYMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIA THEN CONVERTS FACTOR X TO FACTOR XA
CC BY LIMITED PROTEOLYSIS. FACTOR VIIA WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXA IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HETEROIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U77477; AA837326.1; -.
DR HSRP; P08709; 1PAK.
DR MEROPS; S01.215; -.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_T1.
DR InterPro; IPR006209; EGF_T1.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
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DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00010; EGFBL00D.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00179; EGF CA; 1.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00020; TRYP\_Spc; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS01187; EGF CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW Hydrolyse; Serine protease; Blood coagulation; Zymogen; Glycoprotein;  
KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;  
KW EGF-like domain; Repeat; Signal; Hydroxylation.  
FT SIGNAL 1 21  
FT PROPEP 22 39  
FT CHAIN 40 191  
FT CHAIN 192 444  
FT DOMAIN 45 74  
FT DOMAIN 85 121  
FT DOMAIN 126 167  
FT DOMAIN 192 444  
FT SITE 191 192  
FT ACT\_SITE 232 232  
FT ACT\_SITE 281 281  
FT ACT\_SITE 383 383  
FT BINDING 377 377  
FT BINDING 56 61  
FT DISULFID 89 100  
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FT DISULFID 111 120  
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FT DISULFID 137 151  
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FT DISULFID 174 301  
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FT DISULFID 217 233  
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FT MOD\_RES 65 65  
FT MOD\_RES 68 68  
FT MOD\_RES 74 74  
FT MOD\_RES 102 102  
FT CARBOHYD 211 211  
FT CARBOHYD 242 242  
FT CARBOHYD 306 306  
SQ SEQUENCE 444 AA; 49011 MW; 0481ABC4FE5277F8 CRC64;  
Query Match 68.2%; Score 131; DB 1; Length 444;  
Best Local Similarity 52.3%; Pred. No. 3.3e-16;  
Matches 23; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin  
DE conversion accelerator) (Eptacog alfa).  
CN F7.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=86205965; PubMed=3486420;  
RA Hagen F.S., Gray C.L., O'Hara P.J., Grant F.J., Saari G.C.,  
RA Woodbury R.G., Hart C.E., Insley M.Y., Kistiel W., Kurachi K.,  
RA Davie E.W.;  
RT "Characterization of a cDNA coding for human factor VII.";  
RT Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87260948; PubMed=3037537;  
RA O'Hara P.J., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,  
RA Hagen F.S., Murray M.O.;  
RT "Nucleotide sequence of the gene coding for human factor VII, a  
RT vitamin K-dependent protein participating in blood coagulation.";  
RT Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).  
RN [3]  
RP SEQUENCE FROM N.A. AND VARIANTS THR-352; GLN-413 AND LYS-445.  
RA Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,  
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;  
RT Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.  
RN [4]  
RP SEQUENCE OF 61-466 AND POST-TRANSLATIONAL MODIFICATIONS.  
RX MEDLINE=89088153; PubMed=3264725;  
RA Thim L., Bjorn S., Christensen M., Nicolaisen E.M., Lund-Hansen T.,  
RA Pedersen A.H., Hedner U.;  
RT "Amino acid sequence and posttranslational modifications of human  
RT factor VIIa from plasma and transfected baby hamster kidney cells.";  
RT Biochemistry 27:7785-7793(1988).  
RN [5]  
RP CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.  
RX MEDLINE=91250411; PubMed=1904059;  
RA Bjorn S., Foster D.C., Thim L., Wlberg F.C., Christensen M.,  
RA Komiyama Y., Pedersen A.H., Kistiel W.;  
RT "Human plasma and recombinant factor VII. Characterization of O-  
RT glycosylations at serine residues 52 and 60 and effects of site-  
RT directed mutagenesis of serine 52 to alanine.";  
RT J. Biol. Chem. 266:11051-11057(1991).  
RN [6]  
RP STRUCTURE OF CARBOHYDRATE ON SER-112.  
RX MEDLINE=90062160; PubMed=2511201;  
RA Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.,  
RA Shimomishi Y., Iwanaga S.;  
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide  
RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first  
RT epidermal growth factor-like domain of human factors VII and IX and  
RT protein Z and bovine protein Z.";  
RT J. Biol. Chem. 264:20320-20325(1989).  
RN [7]  
RP STRUCTURE OF CARBOHYDRATE ON SER-112.  
RX MEDLINE=91344709; PubMed=2129367;  
RA Iwanaga S., Nishimura H., Kawabata S., Kistiel W., Hase S., Ikenaka T.,  
RA "A new trisaccharide sugar chain linked to a serine residue in the  
RT first EGF-like domain of clotting factors VII and IX and protein Z.";  
RT Adv. Exp. Med. Biol. 281:121-131(1990).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.  
RX MEDLINE=96175641; PubMed=8598903;  
RA Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,  
RA Konigsberg W.H., Nemerson Y., Kirchhofer D.;  
RT "The crystal structure of the complex of blood coagulation factor  
RT VIIa with soluble tissue factor.";  
RT Nature 380:41-46(1996).

[9]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF FVIIA IN COMPLEX WITH TF.  
 RA MEDLINE=99126538; PubMed=9925787;  
 RA Zhang E., St Charles R., Tulinsky A.;  
 RT "Structure of extracellular tissue factor complexed with factor VIIA  
 RT inhibited with a BPT mutant.";  
 RL J. Mol. Biol. 285:2089-2104(1999).  
 RN (10)  
 RP STRUCTURE BY NMR OF 105-145.  
 RA MEDLINE=98367502; PubMed=9692950;  
 RA Murenby A., Finn B.E., Gipeart G.P., Forsen S., Stenflo J.,  
 RA Drakenberg T.;  
 RT "Solution structure of the N-terminal EGF-like domain from human  
 RT factor VII.";  
 RL Biochemistry 37:10605-10615(1998).  
 RN (11)  
 RP VARIANT GLN-364.  
 RA MEDLINE=91300046; PubMed=2070047;  
 RA O'Brien D.P., Gale K.W., Anderson J.S., McVey J.H., Miller G.J.,  
 RA Meade T.W., Tuddenham E.G.D.;  
 RT "Purification and characterization of factor VII 304-Gln: a variant  
 RT molecule with reduced activity isolated from a clinically unaffected  
 RT male.";  
 RL Blood 78:132-140(1991).  
 RN (12)  
 RP VARIANTS GLN-364 AND PHE-370.  
 RA MEDLINE=92340074; PubMed=1634227;  
 RA Marchetti G., Patraccini P., Gemmati D., Derosa V., Pinotti M.,  
 RA Rodorigo G., Casonato A., Girolami A., Bernardi F.;  
 RT "Detection of two missense mutations and characterization of a repeat  
 RT polymorphism in the factor VII gene (F7).";  
 RL Hum. Genet. 89:497-502(1992).  
 RN (13)  
 RP VARIANT TYR-238.  
 RA MEDLINE=93372811; PubMed=8364544;  
 RA Marchetti G., Ferrati M., Patraccini P., Redaelli R., Bernardi F.;  
 RT "A missense mutation (178Cys->Tyr) and two neutral dimorphisms  
 RT (115His and 333Ser) in the human coagulation factor VII gene.";  
 RL Hum. Mol. Genet. 2:1055-1056(1993).  
 RN (14)  
 RP VARIANTS.  
 RA MEDLINE=94061028; PubMed=8242057;  
 RA Takamiya O., Kemball-Cook G., Martin D.M.A., Cooper D.N.,  
 RA von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,  
 RA Tuddenham E.G.D., McVey J.H.;  
 RT "Detection of missense mutations by single-strand conformational  
 RT polymorphism (SSCP) analysis in five dysfunctional variants of  
 RT coagulation factor VII.";  
 RL Hum. Mol. Genet. 2:1355-1359(1993).  
 RN (15)  
 RP VARIANTS CHARLOTTE GLN-139 AND GLN-212.  
 RA MEDLINE=94264305; PubMed=8204879;  
 RA Chaign S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W.,  
 RA Roberts H.R., Blajchman W., Monroe D.W., High K.A.;  
 RT "Severe factor VII deficiency caused by mutations abolishing the  
 RT cleavage site for activation and altering binding to tissue factor.";  
 RL Blood 83:3524-3535(1994).  
 RN (16)  
 RP VARIANT VAL-354.  
 RA MEDLINE=95072589; PubMed=7981691;  
 RA Bernardi F., Caetanani G., Redaelli R., Pinotti M., Lunghi B.,  
 RA Rodeghiero F., Marchetti G.;  
 RT "Topologically equivalent mutations causing dysfunctional coagulation  
 RT factor VII (294Ala->Val) and X (334Ser->Pro).";  
 RL Hum. Mol. Genet. 3:1175-1177(1994).  
 RN (17)  
 RP VARIANT MET HIS-307.  
 RA MEDLINE=95064662; PubMed=7974346;  
 RA Ohwaki M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,  
 RA Suzuki K.;  
 RT "Factor VII: heterozygous asymptomatic type I deficiency caused by  
 RT an amino acid substitution of His (CAC) for Arg(247) (CGC) in the  
 RT catalytic domain.";

RL Thromb. Haemost. 71:773-777(1994).  
 RN (18)  
 RP VARIANT MET-419.  
 RA MEDLINE=96247510; PubMed=8652821;  
 RA Arbini A.A., Mannucci P.M., Bauer K.A.;  
 RT "A Thr35Met mutation in factor VII of a patient with a hereditary  
 RT deficiency causes defective secretion of the molecule.";  
 RL Blood 87:5085-5094(1996).  
 RN (19)  
 RP VARIANTS TRP-283; LYS-325; VAL-358; GLN-364; GLU-402 AND GLN-413.  
 RA MEDLINE=97001216; PubMed=8644208;  
 RA Bernardi F., Caetanani G., Pinotti M., Ferrarese P., di Iasio M.G.,  
 RA Lunghi B., Rodeghiero F., Marchetti G.;  
 RT "Mutation pattern in clinically asymptomatic coagulation factor VII  
 RT deficiency.";  
 RL Hum. Mutat. 8:108-115(1996).  
 RN (20)  
 RP VARIANT VAL-304.  
 RA MEDLINE=97037613; PubMed=8883260;  
 RA Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,  
 RA Brenner B., Paz M., Luder A.S., Blau O., Korostilchevsky M.,  
 RA Zaitov R., Seligson U.;  
 RT "A18244Val is a common, probably ancient mutation causing factor VII  
 RT deficiency in Moroccan and Iranian Jews.";  
 RL Thromb. Haemost. 76:283-291(1996).  
 RN (21)  
 RP VARIANT MORIOKA PRO-13.  
 RA MEDLINE=98235713; PubMed=9576180;  
 RA Ozawa T., Takikawa Y., Niya K., Ejiri N., Suzuki K., Sato S.,  
 RA Sakuragawa N.;  
 RT "Factor VII Moriooka (FVII L-26P): a homozygous missense mutation in  
 RT the signal sequence identified in a patient with factor VII  
 RT deficiency.";  
 RL Br. J. Haematol. 101:47-49(1998).  
 RN (22)  
 RP VARIANTS MALTA THR-194 AND VAL-304.  
 RA MEDLINE=98112461; PubMed=9452082;  
 RA Alshawi C., Scerri C., Galdies R., Aquilina A., Felice A.E.;  
 RT "Two new missense mutations (P134T and A244V) in the coagulation  
 RT factor VII gene.";  
 RL Hum. Mutat. Suppl. 1:S189-S191(1998).  
 RN (23)  
 RP VARIANTS ASP-295 AND GLN-413.  
 RA MEDLINE=99318093; PubMed=10391209;  
 RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,  
 RA Shaw N., Lane C.R., Lm E.P., Kalyanaram N., Nemesh J., Ziaugra L.,  
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,  
 RA Lander E.S.;  
 RT "Characterization of single-nucleotide polymorphisms in coding regions  
 RT of human genes.";  
 RL Nat. Genet. 22:231-238(1999).  
 Query Match 64.1%; Score 123; DB 1; Length 466;  
 Best Local Similarity 52.3%; Pred. No. 1e-14;  
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;  
 Oy 1 ANGFLXLLRQSLXRCRXLLCSFXHXTFRNXXRFRQWVSY 44  
 Db 61 ANAFLELRPSLERBECKEQCSFEARELIFKDAERTKLPWISY 104  
 RESULT 4  
 TMG1\_HUMAN STANDARD; PRT; 218 AA.  
 AC O1468;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Transmembrane gamma-carboxyglutamic acid protein 1 precursor (Proline-  
 DE rich gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein  
 DE 1).  
 GN PRG1 OR TMG1 OR PRG1.  
 OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97404347; PubMed=9256434;
RA Kuhlman J.D., Harris J.B., Haldeman B.A., Davie E.W.;
RT "Primary structure and tissue distribution of two novel proline-rich
RT gamma-carboxyglutamic acid proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
CC -1- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
CC -1- PM: Gla residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF009242; AAB67070.1; -.
DR HSSP; P00740; 1CFH.
DR Genew; HGNC:9469; PRG1.
DR MIM; 604428; -.
DR GO; GO:0005887; C:Integral to plasma membrane; TAS.
DR InterPro; IPR002383; GLA_Blood.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; Gla; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00069; GLA; 1.
DR PROSITE; PS00011; GUU_CARBOXYLATION; 1.
KM Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 20
FT CHAIN 21 218
FT DOMAIN 21 83
FT TRANSMEM 84 106
FT DOMAIN 107 218
FT DOMAIN 24 61
FT DOMAIN 131 135
SQ SEQUENCE 218 AA; 24947 MW; 26538A61BA0A8B98 CRC64;

Query Match 58.9%; Score 113; DB 1; Length 218;
Best Local Similarity 40.9%; Pred. No. 3,1e-13;
Matches 18; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 ANGLXXLRQGSLLKRXCRXXLCSPFXAHXIPRNXXRTROPVNVSY 44
Db 21 ANGFBEIRQGNIRBECKEETBEAREAPENNEKTEKFEWSTY 64

RESULT 5
PRTC MOUSE
ID PRTC_MOUSE STANDARD; PRT; 461 AA.
AC P33587; O35498;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Vitamin-K-dependent protein C precursor (EC 3.4.21.65)
DE (Autoproteolytic cleavage) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92316897; PubMed=1618739;

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RA Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;
RT "Isolation and characterization of a mouse protein C cDNA."
RL J. Biochem. 111:491-495(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RX MEDLINE=98152576; PubMed=9493582;
RA Jalbert L.R., Rosen E.D., Liesens A., Carmeliet P., Collen D.,
RA Castellino F.J.;
RT "Nucleotide structure and characterization of the murine gene encoding
RT anticoagulant protein C."
RL Thromb. Haemost. 79:310-316(1998).
RN [3]
RP SEQUENCE OF 274-434 FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=94318474; PubMed=8043441;
RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Nino Y.;
RT "A comparative study of partial primary structures of the catalytic
RT region of mammalian protein C."
RL Br. J. Haematol. 86:590-600(1994).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIII
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GUU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -----
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CC -----
DR EMBL; D10445; BAA01235.1; -.
DR EMBL; AF034569; AAC33795.1; -.
DR EMBL; D43755; BAA07812.1; -.
DR PIR; JX0210; JX0210.
DR HSSP; P04070; 1PCU.
DR MEROPS; S01.218; -.
DR MGD; MGI:97771; Proc.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_lke.
DR InterPro; IPR002383; GLA_Blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRY_SP; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.

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DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
FT SIGNAL 1 33
FT PROPEP 34 41
FT CHAIN 42 196
FT CHAIN 199 461
FT PEPTIDE 199 212
FT SITE 212 213
FT DOMAIN 96 131
FT DOMAIN 135 175
FT DOMAIN 213 461
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
FT MOD_RES 57 57
FT MOD_RES 60 60
FT MOD_RES 61 61
FT MOD_RES 66 66
FT MOD_RES 67 67
FT MOD_RES 70 70
FT MOD_RES 112 112
FT ACT_SITE 253 253
FT ACT_SITE 299 299
FT ACT_SITE 402 402
FT DISULFID 58 63
FT DISULFID 91 110
FT DISULFID 100 105
FT DISULFID 104 119
FT DISULFID 121 130
FT DISULFID 139 150
FT DISULFID 146 159
FT DISULFID 161 174
FT DISULFID 182 319
FT DISULFID 238 254
FT DISULFID 373 387
FT DISULFID 398 426
FT CARBOHYD 214 214
FT CARBOHYD 290 290
FT CARBOHYD 355 355
FT CONFLICT 328 328
FT CONFLICT 393 393
SQ SEQUENCE 461 AA; 51945 MW; 53PAAOD85B19AD6E CRC64;

Query Match 55.7%; Score 107; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 8.6e-12;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;
QY 1 ANGFLXLRGSLKRXCRXLCSFXAXHIFRNXXRTQFWVSY 44
Db 42 ANSFLEMRPSGLRECHMEICDPEBAQEIFQNVEDTLAFIKY 85

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DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DR Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
DE conversion accelerator).
GN F7 OR CF7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97127167; PubMed=8972017;
RA Idusogie E., Rosen E.D., Carmeliet P., Collen D., Caetzelino F.J.;
RT "Nucleotide structure and characterization of the murine blood
RT coagulation factor VII gene."
RL Thromb. Haemost. 76:957-964 (1996).
CC -1- FUNCTION: CIRCULATES IN THE BLOOD IN A ZMOGEN FORM. FACTOR VII IS
CC CONVERTED TO FACTOR VIIA BY FACTOR XA, FACTOR XIa, FACTOR IXa, OR
CC THROMBIN BY MINOR PROTEOLYSIS. IN THE PRESENCE OF TISSUE FACTOR
CC AND CALCIUM IONS, FACTOR VIIa THEN CONVERTS FACTOR X TO FACTOR Xa
CC BY LIMITED PROTEOLYSIS. FACTOR VIIa WILL ALSO CONVERT FACTOR IX TO
CC FACTOR IXa IN THE PRESENCE OF TISSUE FACTOR AND CALCIUM (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -1- SUBUNIT: HETERODIMER OF A LIGHT CHAIN AND A HEAVY CHAIN LINKED
CC BY A DISULFIDE BOND (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- PTM: THE VITAMIN K-DEPENDENT. ENZYMATIC CARBOXYLATION OF SOME
CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND
CC CALCIUM (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; U66079; AAC3796.1; -.
DR HSSP; P08709; 1BP9.
DR MEROPS; S01.215; -.
DR MGD; MGI:109325; F7.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBLD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00169; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_CA; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS00011; GLU CARBOXYLATION; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrolyase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;

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KM Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;  
 KM EGF-like domain; Repeat; Signal; Hydroxylation.  
 FT SIGNAL 1 24  
 FT PROPEP 25 41  
 FT CHAIN 42 193  
 FT CHAIN 194 446  
 FT DOMAIN 47 76  
 FT DOMAIN 87 123  
 FT DOMAIN 128 169  
 FT DOMAIN 194 446  
 FT SITE 193 194  
 FT ACT\_SITE 234 234  
 FT ACT\_SITE 283 283  
 FT ACT\_SITE 385 385  
 FT BINDING 379 379  
 FT DISULFID 58 63  
 FT DISULFID 91 102  
 FT DISULFID 96 111  
 FT DISULFID 113 122  
 FT DISULFID 132 143  
 FT DISULFID 139 153  
 FT DISULFID 155 168  
 FT DISULFID 176 200  
 FT DISULFID 200 205  
 FT DISULFID 219 235  
 FT DISULFID 351 370  
 FT DISULFID 381 409  
 FT MOD\_RES 47 48  
 FT MOD\_RES 48 48  
 FT MOD\_RES 55 55  
 FT MOD\_RES 57 57  
 FT MOD\_RES 60 60  
 FT MOD\_RES 61 61  
 FT MOD\_RES 66 66  
 FT MOD\_RES 67 67  
 FT MOD\_RES 70 70  
 FT MOD\_RES 76 76  
 FT MOD\_RES 104 104  
 FT CARBOHYD 186 186  
 FT CARBOHYD 244 244  
 FT CARBOHYD 244 244  
 SQ SEQUENCE 446 AA; 50276 MW; 2512E44A45C8C96E CRC64;

Query Match 55.2%; Score 106; DR 1; Length 446;  
 Best Local Similarity 47.7%; Pred. No. 1.3e-11;  
 Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRQGSILKRCXXLCFXAXHIFRNXXRTROFVNSV 44  
 42 ANSLBELWPGSLRECNRECGSEEARLFIKSPERTIKQFIIV 85

RESULT 7  
 PRTC RAT STANDARD; PRT; 461 AA.  
 ID AC P1394;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Vitamin-K-dependent protein C precursor (EC 3.4.21.69)  
 DE (Autoproteolytic cleavage) (Anticoagulant protein C) (Blood coagulation factor XIV).  
 GN PROC.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxId=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Wistar; TISSUE=Liver;  
 RX MEDLINE=92329550; PubMed=1627650;  
 RA Okafuji T., Maekawa K., Nawa K., Marumoto Y.;  
 RT "The cDNA cloning and mRNA expression of rat protein C.";

RL Biochim. Biophys. Acta 1131:329-332(1992).  
 CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT  
 CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA  
 CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.  
 CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va  
 CC and VIIa.  
 CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED  
 CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE  
 CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A  
 CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS IS  
 CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS  
 CC STRONGLY PROMOTED BY THROMBOMODULIN.  
 CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME  
 CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING  
 CC SITE IS NECESSARY FOR THE RECOGNITION OF THE  
 CC THROMBIN-THROMBOMODULIN COMPLEX.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: Contains 2 EGF-like domains.  
 CC -----  
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 CC -----  
 CC EMBL: X64336; CAA45617.1; -;  
 CC PIR: S18994; S18994.  
 CC DR HSSP: P04070, 1PCU.  
 CC DR MEROPS: S01.218; -;  
 CC DR Interpro: IPR000152; Asx hydroxyl.  
 CC DR Interpro: IPR001314; Chymotrypsin.  
 CC DR Interpro: IPR001881; EGF Ca.  
 CC DR Interpro: IPR006209; EGF\_Like.  
 CC DR Interpro: IPR002383; GLA\_Blood.  
 CC DR Interpro: IPR001254; Ser. protease\_Try.  
 CC DR Interpro: IPR000294; VitK\_dep\_GLA.  
 CC DR Pfam: PF00008; EGF\_2.  
 CC DR Pfam: PF00594; Gla; 1.  
 CC DR Pfam: PF00089; trypsin; 1.  
 CC DR PRINTS: PR00722; CHYMOTRYPSIN.  
 CC DR PRINTS: PR00001; GLABLOOD.  
 CC DR SMART: SM00179; EGF\_CA; 1.  
 CC DR SMART: SM00069; GLA; 1.  
 CC DR SMART: SM00020; TRYPSIN\_DOM; 1.  
 CC DR PROSITE: PS00010; ASX\_HYDROXYL; 1.  
 CC DR PROSITE: PS00022; EGF\_1; 1.  
 CC DR PROSITE: PS0186; EGF\_2; 2.  
 CC DR PROSITE: PS0187; EGF\_CA; 1.  
 CC DR PROSITE: PS00011; GLU CARBOXYLATION; 1.  
 CC DR PROSITE: PS00240; TRYPSIN\_DOM; 1.  
 CC DR PROSITE: PS00134; TRYPSIN\_HIS; 1.  
 CC DR PROSITE: PS00135; TRYPSIN\_SER; 1.  
 CC KM Blood coagulation; Glycoprotein; Serine protease;  
 CC KM Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
 CC KM EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.  
 FT SIGNAL 1 32  
 FT PROPEP 33 41  
 FT CHAIN 42 196  
 FT CHAIN 199 461  
 FT PEPTIDE 199 212  
 FT SITE 212 213  
 FT DOMAIN 96 131  
 FT DOMAIN 135 175  
 FT DOMAIN 213 461  
 FT MOD\_RES 47 47  
 FT MOD\_RES 48 48

BY SIMILARITY.  
 BY SIMILARITY.  
 PROTEIN C LIGHT CHAIN (BY SIMILARITY).  
 PROTEIN C HEAVY CHAIN (BY SIMILARITY).  
 ACTIVATION PEPTIDE (BY SIMILARITY).  
 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).  
 EGF-LIKE 1.  
 EGF-LIKE 2.  
 SERINE PROTEASE.  
 GAMMA-CARBOXYGLUTAMIC ACID  
 (BY SIMILARITY).  
 GAMMA-CARBOXYGLUTAMIC ACID  
 (BY SIMILARITY).  
 (BY SIMILARITY).

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FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 57 57 (BY SIMILARITY).
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 61 61 (BY SIMILARITY).
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 66 66 (BY SIMILARITY).
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 67 67 (BY SIMILARITY).
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID
FT MOD_RES 70 70 (BY SIMILARITY).
FT MOD_RES 112 112 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 254 254 CHARGE RELAY SYSTEM.
FT ACT_SITE 300 300 CHARGE RELAY SYSTEM.
FT ACT_SITE 402 402 CHARGE RELAY SYSTEM.
FT DISULFID 58 63 BY SIMILARITY.
FT DISULFID 91 110 BY SIMILARITY.
FT DISULFID 100 105 BY SIMILARITY.
FT DISULFID 104 119 BY SIMILARITY.
FT DISULFID 121 130 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 146 159 BY SIMILARITY.
FT DISULFID 161 174 BY SIMILARITY.
FT DISULFID 182 320 INTERCHAIN (BY SIMILARITY).
FT DISULFID 239 255 BY SIMILARITY.
FT DISULFID 373 387 BY SIMILARITY.
FT DISULFID 398 426 BY SIMILARITY.
FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 461 AA; 51912 MW; 8A4CF93664EDACD5 CRC64;
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Query Match 55.2%; Score 106; DB 1; Length 461;
Best Local Similarity 45.5%; Pred. No. 1.3e-11;
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;
```

```
Oy 1 ANGFLXXLRQSLKRCXKXLCSPFXAHXIFRNXXRTQFWVSY 44
Db 42 ANSFLEELRQGTIERECMEETCSYEVEKVEFENKXETMEFWKGY 85
```

## RESULT 8

```
TMG3_HUMAN STANDARD; PRT; 231 AA.
ID TMG3_HUMAN
```

```
AC Q9BZD7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Transmembrane gamma-carboxyglutamic acid protein 3 precursor.
GN TMG3.
```

```
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
```

```
RT "Identification of two novel transmembrane gamma-carboxyglutamic acid
RT proteins expressed broadly in fetal and adult tissues."
RL Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
```

```
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.
CC -1- PTM: Gla residues are produced after subsequent posttranslational
CC modifications of glutamic acid by a vitamin K-dependent gamma-
CC carboxylase.
```

```
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CC or send an email to license@ebi.ac.uk).
```

```
DR EMBL; AF326350; AAK0955.1; -.
DR HSSP; P00740; ICFH.
DR GO; GO:0016021; C:Integral to membrane; NAS.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR SMART; SM00659; GLA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
KW Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
FT PROPEP 1 19 POTENTIAL.
FT CHAIN 20 231 TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
FT DOMAIN 20 78 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 79 101 POTENTIAL.
FT DOMAIN 102 231 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 23 60 GLA-RICH.
SQ SEQUENCE 231 AA; 25848 MW; 8A373E4848490D81 CRC64;
```

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Query Match 54.7%; Score 105; DB 1; Length 231;
Best Local Similarity 40.9%; Pred. No. 9.6e-12;
Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;
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```
Oy 1 ANGFLXXLRQSLKRCXKXLCSPFXAHXIFRNXXRTQFWVSY 44
Db 20 ANSFLEELRQGTIERECMEETCSYEVEKVEFENKXETMEFWKGY 63
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## RESULT 9

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PRTC_PIG STANDARD; PRT; 459 AA.
ID PRTC_PIG
```

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AC Q9GFP2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysin IIR) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
GN PROC.
```

```
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9623;
```

```
RT "Porcine factor V: cDNA cloning, gene mapping, three-dimensional
RT protein modelling of membrane binding sites and comparative anatomy of
RT domains."
RL Cell. Mol. Life Sci. 58:148-159(2001).
```

```
CC -1- FUNCTION: Protein C is a vitamin K-dependent serine protease that
CC regulates blood coagulation by inactivating factors Va and VIIIa
CC in the presence of calcium ions and phospholipide.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIa.
```

```
CC -1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
CC into a light chain and a heavy chain held together by a disulfide
CC bond. The enzyme is then activated by thrombin, which cleaves a
CC tetradecapeptide from the amino end of the heavy chain; this
CC reaction, which occurs at the surface of endothelial cells, is
CC strongly promoted by thrombomodulin.
```

```
CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -1- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
CC residues allows the modified protein to bind calcium.
CC -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to
CC another site, beyond the GLA domain. This GLA-independent binding
```

CC site is necessary for the recognition of the  
 CC thrombin-thrombomodulin complex.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: Contains 2 EGF-like domains.  
 CC -----  
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 CC -----  
 DR HESBP; AF191307; AAC28380.1; -.  
 DR HESBP; P04070; IPCU.  
 DR MEROPS; S01.218; -.  
 DR InterPro; IPR000152; Aex\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VltK\_dep\_GLA.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00594; G1a; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00181; EGF; 2.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; Tryp\_spec; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.  
 DR PROSITE; PS02040; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Blood coagulation; Glycoprotein; Serine protease;  
 KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;  
 KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.  
 FT SIGNAL 1 18  
 FT PROPEP 19 41  
 FT CHAIN 42 459  
 FT CHAIN 42 196  
 FT CHAIN 199 459  
 FT CHAIN 199 213  
 FT SITE 213 214  
 FT DOMAIN 96 131  
 FT DOMAIN 135 175  
 FT DOMAIN 214 459  
 FT MOD\_RES 47 47  
 FT MOD\_RES 48 48  
 FT MOD\_RES 55 55  
 FT MOD\_RES 57 57  
 FT MOD\_RES 60 60  
 FT MOD\_RES 61 61  
 FT MOD\_RES 66 66  
 FT MOD\_RES 67 67  
 FT MOD\_RES 70 70

FT MOD\_RES 112 112  
 FT ACT\_SITE 255 255  
 FT ACT\_SITE 301 301  
 FT ACT\_SITE 400 400  
 FT DISULFID 58 63  
 FT DISULFID 91 110  
 FT DISULFID 100 105  
 FT DISULFID 104 119  
 FT DISULFID 121 130  
 FT DISULFID 139 150  
 FT DISULFID 146 159  
 FT DISULFID 161 174  
 FT DISULFID 182 321  
 FT DISULFID 240 256  
 FT DISULFID 371 385  
 FT DISULFID 396 424  
 FT CARBOHYD 138 138  
 FT CARBOHYD 292 292  
 FT CARBOHYD 353 353  
 SQ SEQUENCE 459 AA; 51866 MW; 8541AAC14CC16D09 CRC64;  
 Query Match 53.1%; Score 102; DB 1; Length 459;  
 Best Local Similarity 45.5%; Pred. No. 7; Ie-11;  
 Matches 20; Conservative 2; Mismatches 22; Indels 0; Gaps 0;  
 QY 1 ANGFLXKLRGSLRXRCXKXLCSPXXAHKIFRXXXTROQWVSX 44  
 DB 42 ANSFLEELRPSLERCKERTCPDEARLETONTENTAMWSKY 85  
 RESULT 10  
 PRTC\_BOVIN STANDARD; PRT; 456 AA.  
 AC P00745;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Vitamin-K-dependent protein C precursor (BC 3.4.21.69)  
 DE (Autoproteolytic cleavage)  
 DE (Anticoagulant protein C) (Blood coagulation  
 factor XIV) (Fragment).  
 GN PROC.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85014826; PubMed=6091100;  
 RA Long G.L., Balagaje R.M., McGillivray R.T.A.,  
 RT "Cloning and sequencing of liver cDNA coding for bovine protein C";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).  
 RN [2]  
 RP SEQUENCE OF 40-194, AND CARBOHYDRATE-LINKAGE SITE ASN-136.  
 RX MEDLINE=83007325; PubMed=6896876;  
 RA Fernlund P., Stenflo J.,  
 RT "Amino acid sequence of the light chain of bovine protein C";  
 RL J. Biol. Chem. 257:12170-12179(1982).  
 RN [3]  
 RP REVISION TO 110.  
 RX MEDLINE=83169769; PubMed=6572939;  
 RA Drakenberg T., Fernlund P., Koepstorff P., Stenflo J.,  
 RT "Beta-hydroxyaspartic acid in vitamin K-dependent protein C";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).  
 RN [4]  
 RP SEQUENCE OF 197-456, AND CARBOHYDRATE-LINKAGE SITES ASN-289; ASN-350  
 RX AND ASN-366  
 RX MEDLINE=83007326; PubMed=6896877;  
 RA Stenflo J., Fernlund P.,  
 RT "Amino acid sequence of the heavy chain of bovine protein C";  
 RL J. Biol. Chem. 257:12180-12190(1982).  
 RN [5]

```

RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213513; PubMed=6304092;
RA Esmen N.L., Debaule L.E., Esmen C.T.;
RT "Proteolytic formation and properties of gamma-carboxyglutamic acid-
RT domainless protein C.";
RL J. Biol. Chem. 258:5548-5553 (1983).
RN [6]
RP PROCESSING, AND CALCIUM-BINDING DATA.
RX MEDLINE=83213514; PubMed=6406503;
RA Johnson A.E., Esmen N.L., Laue T.M., Esmen C.T.;
RT "Structural changes required for activation of protein C are induced
RT by Ca2+ binding to a high affinity site that does not contain gamma-
RT carboxyglutamic acid.";
RL J. Biol. Chem. 258:5554-5560 (1983).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VIIIA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIA.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMAIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
-----
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CC EMBL; K02435; AAA30685.1; -.
DR PIR; A26250; KXBO.
DR HSSP; P04070; LPCU.
DR MEROPS; S01.218; -.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_Ca; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Glycoprotein; Serine protease;
Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;

```

```

KW EGF-like domain; Repeat; Endothelial cell; Hydrolyase; Signal.
FT NON_TER 1 1
FT SIGNAL <1 29
FT PROPEP 30 39
FT CHAIN 40 194
FT CHAIN 197 456
FT PEPTIDE 197 210
FT DOMAIN 94 129
FT DOMAIN 133 173
FT DOMAIN 211 456
FT MOD_RES 45 45
FT MOD_RES 46 46
FT MOD_RES 53 53
FT MOD_RES 55 55
FT MOD_RES 58 58
FT MOD_RES 59 59
FT MOD_RES 62 62
FT MOD_RES 64 64
FT MOD_RES 65 65
FT MOD_RES 68 68
FT MOD_RES 74 74
FT MOD_RES 110 110
FT ACT_SITE 252 252
FT ACT_SITE 298 298
FT ACT_SITE 397 397
FT DISULFID 56 61
FT DISULFID 89 108
FT DISULFID 98 103
FT DISULFID 102 117
FT DISULFID 119 128
FT DISULFID 137 148
FT DISULFID 144 157
FT DISULFID 159 172
FT DISULFID 180 318
FT DISULFID 237 253
FT DISULFID 368 382
FT DISULFID 393 421
FT CARBOHYD 136 136
FT CARBOHYD 289 289
FT CARBOHYD 350 350
FT CARBOHYD 366 366
FT VARIANT 82 82
FT VARIANT 455 456
FT CONFLICT 455 456
SQ SEQUENCE 456 AA; 51407 MM; CAAFe633F894C209 CRC64;

Query Match 50.5%; Score 97; DB 1; Length 456;
Best Local Similarity 43.2%; Pred. No. 5.8e-10;
Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRQGSILKRCXXLCSPFXAHXIFRNXXRTROPWVSX 44
Db 40 ANSFLEELRGNVRECESEVCFEERARLIFQNTEDIMARSPY 83

RESULT 11
ID FA10_HUMAN STANDARD; PRT; 488 AA.
AC P00742; O14340;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
GN F10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91216473; PubMed=1902434.
RA Wessler T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.;
RT "Cloning and expression in COS-1 cells of a full-length cDNA encoding
RT human coagulation factor X.";

```



RL Gene 99:291-294(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87026600; PubMed=3768336;  
 RA Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;  
 RT "Gene for human factor X: a blood coagulation factor whose gene  
 RT organization is essentially identical with that of factor IX and  
 RT protein C.";  
 RL Biochemistry 25:5098-5102(1986).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Rieder M.J., Armet T.Z., Carrington D.P., Chung M.-W., Lee K.L.,  
 RA Osuna M., Peol C.L., Toth E.J., Yi Q., Nickerson D.A.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 13-488 FROM N.A.  
 RX MEDLINE=85216545; PubMed=2582420;  
 RA Fung M.R., Hay C.W., McGillivray R.T.A.;  
 RT "Characterization of an almost full-length cDNA coding for human  
 RT blood coagulation factor X.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).  
 RN [5]  
 RP SEQUENCE OF 19-488 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=86221713; PubMed=3011603;  
 RA Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;  
 RT "Isolation and characterization of human blood-coagulation factor X  
 RT cDNA.";  
 RL Gene 41:311-314(1986).  
 RN [6]  
 RP SEQUENCE OF 41-179.  
 RX MEDLINE=83257207; PubMed=6871167;  
 RA McMullen B.A., Fujikawa K., Kistiel W., Saegawa T., Howard W.N.,  
 RA Kwa E.Y., Weinstein B.;  
 RT "Complete amino acid sequence of the light chain of human blood  
 RT coagulation factor X: evidence for identification of residue 63 as  
 RT beta-hydroxyaspartic acid.";  
 RL Biochemistry 22:2875-2884(1983).  
 RN [7]  
 RP SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY.  
 RC TISSUE=Liver;  
 RX MEDLINE=84222026; PubMed=6587384;  
 RA Leytus S.P., Chung D.W., Kistiel W., Kurachi K., Davie E.W.;  
 RT "Characterization of a cDNA coding for human factor X.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).  
 RN [8]  
 RP SEQUENCE OF 183-234, AND CARBOHYDRATE-LINKAGE SITES.  
 RX MEDLINE=94062825; PubMed=8243461;  
 RA Inoue K., Morita T.;  
 RT "Identification of O-linked oligosaccharide chains in the activation  
 RT peptides of blood coagulation factor X. The role of the carbohydrate  
 RT moieties in the activation of factor X.";  
 RL Eur. J. Biochem. 218:153-163(1993).  
 RN [9]  
 RP SEQUENCE OF 1-23 FROM N.A.  
 RX MEDLINE=90128299; PubMed=2612918;  
 RA Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhusanam K., Lyman G.;  
 RT "Cloning and characterization of the 5' end (exon 1) of the gene  
 RT encoding human factor X.";  
 RL Gene 84:517-519(1989).  
 RN [10]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=93360277; PubMed=8355279;  
 RA Padmanabhan K.P., Padmanabhan K.P., Tullinsky A., Park C.H., Bode W.,  
 RA Huber R., Blankenship D.T., Cardin A.D., Kistiel W.;  
 RT "Structure of human des(1-45) factor Xa at 2.2-A resolution.";  
 RL J. Mol. Biol. 232:947-966(1993).  
 RN [11]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.  
 RX MEDLINE=98283982; PubMed=9618463;  
 RA Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;  
 RT "Structural basis for chemical inhibition of human blood coagulation  
 RT factor Xa."

RL Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).  
 RN [12]  
 RP VARIANTS ILE-7 AND HIS-30.  
 RX MEDLINE=99318093; PubMed=10391209;  
 RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patel N.,  
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemes J., Ziaagra L.,  
 RA Friedland L., Rolfe A., Warrington J., Lipschutz R., Daley G.O.,  
 RA Lander E.S.;  
 RT "Characterization of single-nucleotide polymorphisms in coding regions  
 RT of human genes.";  
 RL Nat. Genet. 22:231-238(1999).  
 RN [13]  
 RP ERRATUM.  
 RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patel N.,  
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemes J., Ziaagra L.,  
 RA Friedland L., Rolfe A., Warrington J., Lipschutz R., Daley G.O.,  
 RA Lander E.S.;  
 RL Nat. Genet. 23:373-373(1999).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 CC converts prothrombin to thrombin in the presence of factor Va,  
 CC calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 CC Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 CC MORE DISULFIDE BONDS.  
 CC -1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -1- PTM: N- AND O-GLYCOSYLATED.  
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IYA (IN THE  
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: Contains 2 BGF-like domains.  
 CC -----  
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 CC -----  
 DR EMBL, KO3194; AAA52490.1; -;  
 DR EMBL, M57285; AAA52421.1; -;  
 DR EMBL, AF503510; AAM19347.1; -;  
 DR EMBL, L29433; AAA52764.1; -;  
 DR EMBL, L00390; AAA52764.1; JOINED.  
 DR EMBL, L00391; AAA52764.1; JOINED.  
 DR EMBL, L00392; AAA52764.1; JOINED.  
 DR EMBL, L00393; AAA52764.1; JOINED.  
 DR EMBL, L00394; AAA52764.1; JOINED.  
 DR EMBL, L00395; AAA52764.1; JOINED.  
 DR EMBL, L00396; AAA52764.1; JOINED.  
 DR EMBL, M22613; AAA51984.1; -;  
 DR EMBL, K01886; AAA52486.1; -;  
 DR EMBL, M33297; AAA52636.1; -;  
 DR PIR, A24478; EXHU.  
 DR PDB, 1HCG; 08-MAY-95.  
 DR PDB, 1FXJ; 29-OCT-97.  
 DR PDB, 1FXK; 17-JUN-98.  
 DR PDB, 1XKA; 23-MAR-99.  
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 DR PDB, 1XKX; 23-MAR-99.  
 DR PDB, 1EZO; 20-SEP-00.  
 DR PDB, 1FOR; 20-SEP-00.  
 DR PDB, 1FOS; 20-SEP-00.  
 DR PDB, 1FUS; 17-NOV-00.  
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 DR PDB, 1KSN; 19-JUN-02.  
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 DR PDB, 1MO5; 28-JAN-03.

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DR PDB; 1WQ6; 28-JAN-03.
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DR PDB; 1NFV; 25-FEB-03.
DR PDB; 1NFY; 25-FEB-03.
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DR GlycoSuiteDB; P00742; -.
DR Genew; HGNC:3528; F10.
DR MIM; 134530; -.
DR MIM; 227600; -.
DR GO; GO:0005576; C:extracellular; TAS.
DR GO; GO:0003804; F:blood coagulation factor X activity; TAS.
DR GO; GO:0007356; P:blood coagulation; TAS.
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DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR00138; EGF_11.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; trypsin; 1.
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DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00001; GLABLOOD.
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DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRY_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.

Query March 50.0%; Score 96; DB 1; Length 488;
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Db 41 ANSFLEBKXGHLSECMETCSYEAREVEVDSKTNFNNKY 84

RESULT 12
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DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
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GN F10.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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RX MEDLINE=84247315; PubMed=6330671;
RA Fung M.R., Campbell R.M., McGillivray R.T.A.;
RT "Blood coagulation factor X mRNA encodes a single polypeptide chain
RT containing a prepro leader sequence.";
RL Nucleic Acids Res. 12:4481-4492(1984).
RN [2]
RP SEQUENCE OF 41-180.
RX MEDLINE=80130563; PubMed=6766735;
RA Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
RA Titani K.;

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RT "Amino acid sequence of the light chain of bovine factor XI (Stuart
RT factor).";
RL Biochemistry 19:659-667(1980).
RN [3]
RP REVISION TO 103.
RX MEDLINE=83308813; PubMed=6685526;
RA McMullen B.A., Fujikawa K., Kisiel W.;
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin
RT K-dependent blood coagulation zymogens.";
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).
RN [4]
RP SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX MEDLINE=76053069; PubMed=1059093;
RA Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
RA Neurath H.;
RT "Bovine factor XI (Stuart factor): amino-acid sequence of heavy
RT chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).
RN [5]
RP SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=94062825; PubMed=8243461;
RA Inoue K., Morita T.;
RT "Identification of O-linked oligosaccharide chains in the activation
RT peptides of blood coagulation factor X. The role of the carbohydrate
RT moieties in the activation of factor X.";
RL Eur. J. Biochem. 218:153-163(1993).
RN [6]
RP ACTIVE SITE.
RX MEDLINE=73053314; PubMed=4264286;
RA Titani K., Hermanson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
RA Neurath H., Davie E.W.;
RT "Bovine factor X 1a (activated Stuart factor). Evidence of homology
RT with mammalian serine proteases.";
RL Biochemistry 11:4899-4903(1972).
RN [7]
RP PROCESSING.
RX MEDLINE=76053121; PubMed=1059122;
RA Fujikawa K., Titani K., Davie E.W.;
RT "Activation of bovine factor X (Stuart factor): conversion of factor
RT Xa-alpha to factor Xa-beta.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
RN [8]
RP CALCIUM-BINDING DATA.
RX MEDLINE=84185716; PubMed=6546930;
RA Suo T., Björk I., Holmgren A., Stenflo J.;
RT "Calcium-binding properties of bovine factor X lacking the gamma-
RT carboxyglutamic acid-containing region.";
RL J. Biol. Chem. 259:5705-5710(1984).
RN [9]
RP SUBUNIT.
RX MEDLINE=86140210; PubMed=3949800;
RA Morita T., Jackson C.M.;
RT "Localization of the structural difference between bovine blood
RT coagulation factors XI and XII to tyrosine 18 in the activation
RT peptide.";
RL J. Biol. Chem. 261:4008-4014(1986).
RN [10]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=91084483; PubMed=2261466;
RA Selander M., Persson E., Stenflo J., Drakenberg T.;
RT "1H NMR assignment and secondary structure of the Ca2(+)-free form of
RT the amino-terminal epidermal growth factor like domain in coagulation
RT factor X.";
RL Biochemistry 29:8111-8118(1990).
RN [11]
RP STRUCTURE BY NMR OF 85-126.
RX MEDLINE=92329412; PubMed=1627540;
RA Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
RA Telemann O.;
RT "Three-dimensional structure of the apo form of the N-terminal
RT EGF-like module of blood coagulation factor X as determined by NMR
RT spectroscopy and simulated folding.";
RL Biochemistry 31:5974-5983(1992).

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RN [12]  
 RP STRUCTURE BY NMR OF 85-126.  
 RX MEDLINE=92406922; PubMed=1527084;  
 RA Selander-Sunneberg M., Ullner M., Persson E., Teleman O.,  
 RA Stenflo J., Drakenberg T.,  
 RT "How an epidermal growth factor (EGF)-like domain binds calcium. High  
 RT resolution NMR structure of the calcium form of the NH2-terminal EGF-  
 RT like domain in coagulation factor X.",  
 RL J. Biol. Chem. 267:19642-19649(1992).  
 RN [13]  
 RP STRUCTURE BY NMR OF 41-126.  
 RX MEDLINE=96387194; PubMed=8794734;  
 RA Sunneberg M., Olaf G.A., Stenflo J., Forssen S., Drakenberg T.,  
 RA Trewhella J.,  
 RT "The relative orientation of Gla and EGF domains in coagulation  
 RT factor X is altered by Ca<sup>2+</sup> binding to the first EGF domain. A  
 RT combined NMR-small angle X-ray scattering study.",  
 RL Biochemistry 35:11547-11559(1996).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 CC converts prothrombin to thrombin in the presence of factor Va,  
 CC calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 CC Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 CC MORE DISULFIDE BONDS.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM.  
 CC -1- PTM: N- AND O-GLYCOSYLATED.  
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY).  
 CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO  
 CC ANOTHER SITE, BEYOND THE GLA DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 CC -1- SIMILARITY: Contains 2 EGF-like domains.  
 CC -----  
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 DR PDB: 1KIG; 28-OCT-98.  
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 DR InterPro: IPR000742; EGF\_2.  
 DR InterPro: IPR001881; EGF\_Ca.  
 DR InterPro: IPR006209; EGF\_Like.  
 DR InterPro: IPR002383; GLA\_Like.  
 DR InterPro: IPR001254; Ser\_protease\_Try.  
 DR InterPro: IPR000294; VitK\_dep\_GLA.  
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 DR Pfam; PF00594; gla; 1.  
 DR Pfam; PF00089; trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
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 DR PROSITE; PS00022; EGF\_1; 1.

DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
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 DR PROSITE; PSS0240; TRYPSIN\_DOM; 1.  
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 AC 019045;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).  
 GN F10.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 RX MEDLINE=97256311; PubMed=9101642;  
 RA Pendutht U.R., Anderson K.D., James H.L.,  
 RT "Characterization of a full-length cDNA for rabbit factor X.",  
 RL Thromb. Res. 85:503-514(1997).  
 CC -1- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that  
 CC converts prothrombin to thrombin in the presence of factor Va,  
 CC calcium and phospholipid during blood clotting.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then  
 CC Arg-|-Ile bonds in prothrombin to form thrombin.  
 CC -1- SUBUNIT: THE TWO CHAINS ARE FORMED FROM A SINGLE-CHAIN PRECURSOR  
 CC BY THE EXCISION OF TWO ARG RESIDUES AND ARE HELD TOGETHER BY 1 OR  
 CC MORE DISULFIDE BONDS.  
 CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME  
 CC GLUTAMIC ACID RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND  
 CC CALCIUM (BY SIMILARITY).  
 CC -1- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).  
 CC -1- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE  
 CC INTRINSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)

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CC (BY SIMILARITY).
CC -1- MISCELLANEOUS; CALCIUM ALSO BINDS. WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -----
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CC or send an email to license@isb-sib.ch).
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DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; Vitk_dep_GLA.
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DR Pfam; PF00594; gla; 1.
DR SMART; SM00089; trypsin; 1.
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DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
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DR PROSITE; PS00135; TRYPSIN_SER; 1.
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KW Gamma-carboxyglutamic acid; Hydroxylation; Calcium-binding; Vitamin K;
KW Signal; Zymogen; EGF-like domain; Repeat.
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DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
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GN F9.
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RX MEDLINE=86000558; PubMed=2994716;
RA Yoshitake S., Schach B.G., Foster D.C., Davie E.W., Kurachi K.;
RT "Nucleotide sequence of the gene for human factor IX (antihemophilic
RT factor B).";
RL Biochemistry 24:3736-3750(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85190593; PubMed=3857619;
RA McGraw R.A., Davis L.M., Noyes C.M., Lundblad R.L., Roberts H.R.,
RA Graham J.B., Stafford D.W.;
RT "Evidence for a prevalent dimorphism in the activation peptide of
RT human coagulation factor IX.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:2847-2851(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=84236100; PubMed=6329734;
RA Anson D.S., Choo K.H., Rees D.J.G., Giannelli F., Gould K.G.,
RA Huddleston J.A., Brownlee G.G.;
RT "The gene structure of human anti-haemophilic factor IX.";
RL EMBO J. 3:1053-1060(1984).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=83220788; PubMed=6687940;

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RA Jaye M., de la Salle H., Schamber F., Balland A., Kohli V.,  
RA Finkel A., Tolstoshev P., Lecocq J.P.;  
RT "Isolation of a human anti-haemophilic factor IX cDNA clone using a  
RT unique 52-base synthetic oligonucleotide probe deduced from the amino  
RT acid sequence of bovine factor IX.";  
RL Nucleic Acids Res. 11:2325-2335(1983).  
RN [5]  
RP SEQUENCE FROM N.A., AND VARIANTS THR-194 AND PRO-461.  
RA Rieder M.J., Arnel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,  
RA Rajkumar N.R., Toth E.J., Yi Q., Nickerson D.A.;  
RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE OF 36-326 FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=84300526; PubMed=6089357;  
RA Jagadeeswaran P., Lavelle D.E., Kaul R., Mohandas T., Warren S.T.;  
RT "Isolation and characterization of human factor IX cDNA:  
RT identification of Tag I polymorphism and regional assignment.";  
RL Somat. Cell Mol. Genet. 10:465-473(1984).  
RN [7]  
RP SEQUENCE OF 290-359 FROM N.A.  
RX MEDLINE=88127096; PubMed=3340835;  
RA Scofield E.S., Koebler D.D., Sarkar G., Sommer S.S.;  
RT "Genomic amplification with transcript sequencing.";  
RL Science 239:491-494(1988).  
RN [8]  
RP SEQUENCE OF 444-461 FROM N.A.  
RX MEDLINE=94054330; PubMed=8236150;  
RA de la Salle C., Charmanlier J.L., Baas M.J., Schwartz A.,  
RA Wiesel M.L., Grunbaum L., Cazenave J.-P.;  
RT "A deletion located in the 3' non translated part of the factor IX  
RT gene responsible for mild haemophilia B.";  
RL Thromb. Haemost. 70:370-371(1993).  
RN [9]  
RP SEQUENCE OF 47-461 (VARIANT NAGOYA).  
RX MEDLINE=90078229; PubMed=2592373;  
RA Suehito K., Kawabata S.-I., Miyata T., Takeya H., Takamatsu J.,  
RA Oota K., Kamiya T., Saito H., Niho Y., Iwanaga S.;  
RT "Blood clotting factor IX BM Nagoya. Substitution of arginine 180 by  
RT tryptophan and its activation by alpha-chymotrypsin and rat mast cell  
RT chymase.";  
RL J. Biol. Chem. 264:21257-21265(1989).  
RN [10]  
RP HYDROXYLATION OF ASP-110.  
RX MEDLINE=83308813; PubMed=6688526;  
RA McMullen B.A., Fujikawa K., Kissel W.;  
RT "The occurrence of beta-hydroxyaspartic acid in the vitamin  
RT K-dependent blood coagulation zymogens.";  
RL Biochem. Biophys. Res. Commun. 115:8-14(1983).  
RN [11]  
RP PROCESSING, ACTIVE SITE, AND CARBOHYDRATE-LINKAGE SITES.  
RX MEDLINE=78194509; PubMed=659613;  
RA di Sciopio R.G., Kurachi K., Davie E.W.;  
RT "Activation of human factor IX (Christmas factor).";  
RL J. Clin. Invest. 61:1528-1538(1978).  
RN [12]  
RP CALCIUM-BINDING DATA.  
RX MEDLINE=84185715; PubMed=6425296;  
RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;  
RT "Derivatives of blood coagulation factor IX contain a high affinity  
RT Ca2+-binding site that lacks gamma-carboxyglutamic acid.";  
RL J. Biol. Chem. 259:5698-5704(1984).  
RN [13]  
RP ERRATUM.  
RA Morita T., Isaacs B.S., Esmon C.T., Johnson A.E.;  
RL J. Biol. Chem. 260:2583-2583(1985).  
RN [14]  
RP SIGNAL SEQUENCE CLEAVAGE SITE.  
RX MEDLINE=86189947; PubMed=3009923;  
RA Bentley A.K., Rees D.U.G., Rizza C., Brownlee G.G.;  
RT "Defective propeptide processing of blood clotting factor IX caused  
RT by mutation of arginine to glutamine at position -4.";  
RL Cell 45:343-348(1986).  
RN [15]  
RP STRUCTURE OF CARBOHYDRATE ON SER-99.  
RX MEDLINE=9062160; PubMed=2511201;  
RA Nishimura H., Kawabata S., Kissel W., Hase S., Ikenaka T., Takao T.,  
RA Shimomura Y., Iwanaga S.;  
RT "Identification of a disaccharide (Xyl-Glc) and a trisaccharide  
RT (Xyl2-Glc) O-glycosidically linked to a serine residue in the first  
RT epidermal growth factor-like domain of human factors VII and IX and  
RT protein Z and bovine protein Z.";  
RL J. Biol. Chem. 264:20320-20325(1989).  
RN [16]  
RP STRUCTURE OF CARBOHYDRATE ON SER-99.  
RX MEDLINE=91344709; PubMed=2129367;  
RA Iwanaga S., Nishimura H., Kawabata S., Kissel W., Hase S., Ikenaka T.,  
RT "A new trisaccharide sugar chain linked to a serine residue in the  
RT first EGF-like domain of clotting factors VII and IX and protein Z.";  
RL Adv. Exp. Med. Biol. 281:121-131(1990).  
RN [17]  
RP STRUCTURE OF CARBOHYDRATE ON SER-107.  
RX MEDLINE=92388094; PubMed=1517205;  
RA Nishimura H., Takao T., Hase S., Shimomura Y., Iwanaga S.;  
RT "Human factor IX has a tetrasaccharide O-glycosidically linked to  
RT serine 61 through the fucose residue.";  
RL J. Biol. Chem. 267:17520-17525(1992).  
RN [18]  
RP PHOSPHORYLATION OF SER-114.  
RA Harris R.J., Papac D.I., Truong L., Smith K.J.;  
RT "Partial phosphorylation of serine-68 in EGF-1 of human factor IX.";  
RL (in) Abstracts of 11th international conference on methods in protein  
RN structure analysis, pp.50-50, Annecy (1996).  
RP POST-TRANSLATIONAL MODIFICATIONS.  
RX MEDLINE=20575397; PubMed=11133752;  
RA Arruda V.R., Hagstrom J.N., Delch J., Heiman-Patterson T.,  
RA Camire R.M., Chu K., Fields P.A., Herzog R.W., Couto L.B.,  
RA Larson P.J., High K.A.;  
RT "Posttranslational modifications of recombinant mycrobe-synthesized  
RT human factor IX.";  
RL Blood 97:130-138(2001).  
RN [20]  
RP STRUCTURE BY NMR OF 47-93.  
RX MEDLINE=95229607; PubMed=7713897;  
RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;  
RT "Structure of the metal-free gamma-carboxyglutamic acid-rich membrane  
RT binding region of factor IX by two-dimensional NMR spectroscopy.";  
RL J. Biol. Chem. 270:7980-7987(1995).  
RN [21]  
RP STRUCTURE BY NMR OF 47-93.  
RX MEDLINE=96032604; PubMed=7547952;  
RA Freedman S.J., Furie B.C., Furie B., Baleja J.D.;  
RT "Structure of the calcium ion-bound gamma-carboxyglutamic acid-rich  
RT domain of factor IX.";  
RL Biochemistry 34:12126-12137(1995).  
RN [22]  
RP STRUCTURE BY NMR OF 47-93.  
RX MEDLINE=96279169; PubMed=8663165;  
RA Freedman S.J., Blostein M.D., Baleja J.D., Jacobs M., Furie B.C.,  
RA Furie B.;  
RT "Identification of the phospholipid binding site in the vitamin K-  
RT dependent blood coagulation protein factor IX.";  
RL J. Biol. Chem. 271:16227-16236(1996).  
RN [23]  
RP STRUCTURE BY NMR OF 47-93.  
RX MEDLINE=97199336; PubMed=9047312;  
RA Li L., Darden T.A., Freedman S.J., Furie B.C., Furie B., Baleja J.D.,  
RA Smith H., Hickey R.G., Pedersen L.G.;  
RT "Refinement of the NMR solution structure of the  
RT gamma-carboxyglutamic acid domain of coagulation factor IX using  
RT molecular dynamics simulation with initial Ca2+ positions determined  
RT by a genetic algorithm.";  
RL Biochemistry 36:2132-2138(1997).  
RN [24]  
RP STRUCTURE BY NMR OF 91-133.

RX MEDLINE=91308127; PubMed=1854745;  
 RA Huang L.H., Cheng H., Pardi A., Tam J.P., Sweeney W.V.;  
 RT "Sequence-specific 1H NMR assignments, secondary structure, and  
 RT location of the calcium binding site in the first epidermal growth  
 RT factor like domain of blood coagulation factor IX.";  
 RL Biochemistry 30:7402-7409(1991).  
 RN [25]  
 RP STRUCTURE BY NMR OF 92-130.  
 RX MEDLINE=93284090; PubMed=1304885;  
 RA Bacon M., Norman D.G., Harvey T.S., Handford P.A., Mayhew M.,  
 RA Tse A.G.D., Brownlee G.G., Campbell I.D.C.;  
 RT "The three-dimensional structure of the first EGF-like module of  
 RT human factor IX: comparison with EGF and TGF-alpha.";  
 RL Protein Sci. 1:81-90(1992).  
 RN [26]  
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 92-130.  
 RX MEDLINE=95330802; PubMed=7606779;  
 RA Rao Z., Handford P., Mayhew M., Knott V., Brownlee G.G., Stuart D.;  
 QY 2 NGFLXLRQGSIXRCXRLGSEFXAXHIFRXXTTQFWWSY 44  
 DB 49 SGKLEFVQGNLERCEMEKCSFEERAREVENTERTTEFWKQY 91  
 Query Match 48.4%; Score 93; DB 1; Length 461;  
 Best Local Similarity 41.9%; Pred. No. 3.2e-09;  
 Matches 18; Conservative 4; Mismatches 22; Indels 0; Gaps 0;  
 RESULT 15  
 PRTC HUMAN STANDARD; PRT; 461 AA.  
 AC P04070; Q15189; Q15190; Q16001;  
 DT 01-NOV-1986 (Rel. 03, Created)  
 DT 01-NOV-1986 (Rel. 03, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Vitamin-K-dependent protein C precursor (EC 3.4.21.69)  
 DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation  
 DE factor XIV).  
 GN PROC.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85270390; PubMed=2991887;  
 RA Foster D.C., Yoshitake S., Davie E.W.;  
 RT "The nucleotide sequence of the gene for human protein C.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:4673-4677(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85269639; PubMed=2991859;  
 RA Beckmann R.J., Schmidt R.J., Santerre R.F., Plutsky J., Crabtree G.R.,  
 RA Long G.L.;  
 RT "The structure and evolution of a 461 amino acid human protein C  
 RT precursor and its messenger RNA, based upon the DNA sequence of  
 RT cloned human liver cDNAs.";  
 RL Nucleic Acids Res. 13:5233-5247(1985).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86120978; PubMed=351171;  
 RA Plutsky J., Hosking J.A., Long G.L., Crabtree G.R.;  
 RT "Evolution and organization of the human protein C gene.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:546-550(1986).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,  
 RA Nickerson D.A.;  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 106-461 FROM N.A.  
 RX MEDLINE=84272714; PubMed=6589623;  
 RA Foster D.C., Davie E.W.;

RT "Characterization of a cDNA coding for human protein C.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).  
 RN [6]  
 RP CARBOHYDRATE-LINKAGE SITE ASN-371.  
 RX MEDLINE=90293094; PubMed=1694179;  
 RA Mielich J.P., Broze G.J. Jr.;  
 RT "Beta protein C is not glycosylated at asparagine 329. The rate of  
 RT translation may influence the frequency of usage at asparagine-X-  
 RT cysteine sites.";  
 RL J. Biol. Chem. 265:11397-11404(1990).  
 RN [7]  
 RP HYDROXYLATION.  
 RX MEDLINE=92184750; PubMed=1544894;  
 RA Harris R.J., Ling V.T., Spellman M.W.;  
 RT "O-linked fucose is present in the first epidermal growth factor  
 RT domain of factor XII but not protein C.";  
 RL J. Biol. Chem. 267:5102-5107(1992).  
 RN [8]  
 RP 3D-STRUCTURE MODELING OF 175-450.  
 RX MEDLINE=94272342; PubMed=8003977;  
 RA Fisher C.L., Greengard J.S., Grifflin J.H.;  
 RT "Models of the serine protease domain of the human antithrombotic  
 RT plasma factor activated protein C and its zymogen.";  
 RL Protein Sci. 3:588-599(1994).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.  
 RX MEDLINE=97157472; PubMed=9003757;  
 RA Mather T., Oganessyan V., Hof P., Huber R., Foundling S., Esmen C.,  
 RA Bode W.;  
 RT "The 2.8 A crystal structure of Glu-domainless activated protein C.";  
 RL EMBO J. 15:6822-6831(1996).  
 RN [10]  
 RP REVIEW ON PROC VARIANTS.  
 RX MEDLINE=93190290; PubMed=8446940;  
 RA Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,  
 RA Sala N., Cooper D.N.;  
 RT "Protein C deficiency: a database of mutations. For the Protein C & S  
 RT Subcommittee of the Scientific and Standardization Committee of the  
 RT International Society on Thrombosis and Hemostasis.";  
 RL Thromb. Haemost. 69:77-84(1993).  
 RN [11]  
 RP VARIANT CYS-444.  
 RX MEDLINE=87204221; PubMed=2437584;  
 RA Romeo G., Haasan H.J., Staempfli S., Roncuzzi L., Cianetti L.,  
 RA Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,  
 RA Cortese R.;  
 RT "Hereditary thrombophilia. Identification of nonsense and missense  
 RT mutations in the protein C gene.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).  
 RN [12]  
 RP VARIANT TRP-211 (LONDON-1).  
 RX MEDLINE=90098906; PubMed=2602169;  
 RA Grundy C.B., Chittolile A., Talbot S., Bevan D., Kakkar V.V.,  
 RA Cooper D.N.;  
 RT "Protein C London 1: recurrent mutation at Arg-169 (CGG-->TGG) in  
 RT the protein C gene causing thrombosis.";  
 RL Nucleic Acids Res. 17:10513-10513(1989).  
 RN [13]  
 RP VARIANT CYS-272.  
 RX MEDLINE=91329836; PubMed=1868249;  
 RA Reitsma P.H., Poort S.R., Allaart C.F., Briet E., Bertina R.M.;  
 RT "The spectrum of genetic defects in a panel of 40 Dutch families with  
 RT symptomatic protein C deficiency type I: heterogeneity and founder  
 RT effects.";  
 RL Blood 78:890-894(1991).  
 RN [14]  
 RP VARIANTS ALA-62 (VERMONT-1) AND MET-76.  
 RX MEDLINE=92190481; PubMed=1347706;  
 RA Boviell E.G., Tomczak J.A., Grant B., Bhushan F., Pillemer E.,  
 RA Ratnville I.R., Long G.L.;  
 RT "Protein C Vermont: symptomatic type II protein C deficiency  
 RT associated with two Glu domain mutations.";  
 RL Blood 79:1456-1465(1992).

RN [15]  
 RP VARIANT ASP-418 (HONG KONG-2).  
 RX MEDLINE=92305321; PubMed=1611081;  
 RA Suwahara Y., Miura O., Yuen P., Aoki N.;  
 RT "Protein C deficiency Hong Kong 1 and 2: hereditary protein C  
 RT deficiency caused by two mutant alleles, a 5-nucleotide deletion and  
 RT a missense mutation.";  
 RL Blood 80:126-133(1992).  
 RN [16]  
 RP VARIANT LEU-289.  
 RX MEDLINE=92380660; PubMed=1511988;  
 RA Grundy C.B., Christolm M., Kakkar V.V., Cooper D.N.;  
 RT "A novel homozygous missense mutation in the protein C (PROC) gene  
 RT causing recurrent venous thrombosis.";  
 RL Hum. Genet. 89:683-684(1992).  
 RN [17]  
 RP VARIANTS GLN-220 AND TRP-220.  
 RX MEDLINE=92380661; PubMed=1511989;  
 RA Grundy C.B., Schulman S., Tengborn L., Kakkar V.V., Cooper D.N.;  
 RT "Two different missense mutations at Arg 178 of the protein C (PROC)  
 RT gene causing recurrent venous thrombosis.";  
 RL Hum. Genet. 89:685-686(1992).  
 RN [18]  
 RP VARIANT GLN-220.  
 RX MEDLINE=92350852; PubMed=1301959;  
 RA Gandrille S., Vidaud M., Alach M., Alhenc-Gelas M., Fischer A.M.,  
 RA Gouault-Heilman M., Toulon P., Flessinger J.N., Goossens M.;  
 RT "Two novel mutations responsible for hereditary type I protein C  
 RT deficiency: characterization by denaturing gradient gel  
 RT electrophoresis.";  
 RL Hum. Mutat. 1:491-500(1992).  
 RN [19]  
 RP VARIANT SER-334.  
 RX MEDLINE=92276939; PubMed=1593215;  
 RA Yamamoto K., Matsushita T., Sugitara I., Takamatsu J., Iwasaki E.,  
 RA Wada H., Deguchi K., Shirakawa S., Saito H.;  
 RT "Homozygous protein C deficiency: identification of a novel missense  
 RT mutation that causes impaired secretion of the mutant protein C.";  
 RL J. Lab. Clin. Med. 119:682-689(1992).  
 RN [20]  
 RP VARIANTS TRP-38; CYS-42; HIS-42; GLN-271 AND ASN-294.  
 RX MEDLINE=93313192; PubMed=8324221;  
 RA Gandrille S., Alhenc-Gelas M., Gausem P., Aillaud M.-F., Dupuy E.,  
 RA Juhan-Vaque I., Alach M.;  
 RT "Five novel mutations located in exons III and IX of the protein C  
 RT gene in patients presenting with defective protein C anticoagulant  
 RT activity.";  
 RL Blood 82:159-168(1993).  
 RN [21]  
 RP VARIANTS GLY-14; GLN-211; TYR-244; GLN-253; LEU-321; CYS-328; ILE-385;  
 RP THR-388 AND VAL-388.  
 RX MEDLINE=93271391; PubMed=8499565;  
 RA Poort S.R., Pabinger-Fasching I., Mannhalter C., Reltzma P.H.,  
 RA Bertina R.M.;  
 RT "Twelve novel and two recurrent mutations in 14 Austrian families  
 RT with hereditary protein C deficiency.";  
 RL Blood Coagul. Fibrinolysis 4:273-280(1993).  
 RN [22]  
 RP VARIANT TRP-57.  
 RX MEDLINE=93271396; PubMed=8499568;  
 RA Millar D.S., Grundy C.B., Bignell P., Moffat E.H., Martin R.,  
 RA Kakkar V.V., Cooper D.N.;  
 RT "A Gla domain mutation (Arg 15-->Trp) in the protein C (PROC) gene  
 RT causing type 2 protein C deficiency and recurrent venous  
 RT thrombosis.";  
 RL Blood Coagul. Fibrinolysis 4:345-347(1993).  
 RN [23]  
 RP VARIANTS ARG-145; LEU-210; TRP-211; THR-243; LEU-321; MET-340 AND  
 RP TYR-426.  
 RX MEDLINE=94123239; PubMed=8292730;  
 RA Tsay W., Greengard J.S., Montgomery R.R., McPherson R.A., Fucci J.C.,  
 RA Koerber M.A., Coughlin J., Griffin J.H.;  
 RT "Genetic mutations in ten unrelated American patients with

RT symptomatic type 1 protein C deficiency.";  
 RL Blood Coagul. Fibrinolysis 4:791-796(1993).  
 RN [24]  
 RP VARIANT SER-423.  
 RX MEDLINE=94001606; PubMed=8398832;  
 RA Marchetti G., Patrascu P., Gemmati D., Caetaman G., Rodeghiero F.,  
 RA Wacey A., Cooper D.N., Tuddenham E.G., Bernardi F.;  
 RT "Symptomatic type II protein C deficiency caused by a missense  
 RT mutation (Gly 381-->Ser) in the substrate-binding pocket.";  
 RL Br. J. Haematol. 84:285-289(1993).  
 RN [25]  
 Query Match 47.4%; Score 91; DB 1; Length 461;  
 Best Local Similarity 46.3%; Pred. No. 7.4e-09;  
 Matches 19; Conservative 2; Mismatches 20; Indels 0; Gaps 0;  
 Oy 1 ANGFLXXLRGSLXRYCRXXLCSFPXAXHIFRXXXTROFW 41  
 Db 43 ANSFLELRHSSLERECIERICDFEBAKEIFQWVDTLAFW 83  
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 Job time : 14.5 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 28, 2003, 12:21:25 ; Search time 61 Seconds  
(without alignments)  
186.136 Million cell updates/sec

Title: SEQ4  
Perfect score: 192  
Sequence: 1 ANGFLXXLRGSLXRCRX.....XXAHXIFRNXXRTQFWVSY 44

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_23:\*

1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123	64.1	701	Q96P08	Q96P08 homo sapien
2	113	58.9	268	Q8NEK6	Q8NEK6 homo sapien
3	107	55.7	460	Q91WN8	Q91WN8 mus musculu
4	106	55.2	229	13 Q8J740	Q8J740 xenopus lae
5	105	55.2	446	11 Q61109	Q61109 mus musculu
6	105	54.7	231	4 Q8N2N6	Q8N2N6 homo sapien
7	105	54.7	443	13 Q8JHC9	Q8JHC9 brachydanto
8	101	52.6	460	11 Q99PC6	Q99PC6 mus musculu
9	98	51.0	446	11 Q8K3U6	Q8K3U6 ratu
10	98	51.0	456	6 Q9TR0	Q9TR0 canis fami
11	96	50.0	482	4 Q63207	Q63207 ratu
12	93	48.4	456	4 Q14316	Q14316 homo sapien
13	93	48.4	461	6 Q95ND7	Q95ND7 pan troglod
14	93	48.4	461	6 Q95ND6	Q95ND6 pan troglod
15	93	48.4	481	11 Q54740	Q54740 mus musculu
16	93	48.4	481	11 Q99L32	Q99L32 mus musculu

17	93	48.4	481	11 Q88947	Q88947 mus musculu
18	89	46.4	49	6 Q95ME8	Q95ME8 bos taurus
19	89	46.4	469	6 Q9GMD9	Q9GMD9 ornithothym
20	82	42.7	138	6 Q28994	Q28994 sus scrofa
21	80	41.7	100	4 Q15253	Q15253 homo sapien
22	80	41.7	433	13 Q8JHD0	Q8JHD0 brachydanto
23	80	41.7	433	13 Q90YK1	Q90YK1 brachydanto
24	80	41.7	608	13 Q9PTW7	Q9PTW7 struthio ca
25	80	41.7	648	6 Q29094	Q29094 sus scrofa
26	79	41.1	241	11 Q8C101	Q8C101 mus musculu
27	79	41.1	399	11 Q9CQW3	Q9CQW3 mus musculu
28	77	40.1	55	4 Q8J002	Q8J002 homo sapien
29	77	40.1	55	4 Q8IXB5	Q8IXB5 homo sapien
30	76.5	39.6	542	5 Q8T613	Q8T613 halocynthia
31	75	39.6	474	13 Q8JHC8	Q8JHC8 brachydanto
32	75	39.1	650	4 Q16519	Q16519 homo sapien
33	75	39.1	650	4 Q9NSD0	Q9NSD0 homo sapien
34	71	37.0	179	4 Q8TAS3	Q8TAS3 homo sapien
35	71	37.0	198	11 Q8R182	Q8R182 mus musculu
36	68	35.4	376	13 P83370	P83370 hoplocephal
37	68	35.4	607	13 Q91001	Q91001 gallus gall
38	66	34.4	503	13 Q8AYE4	Q8AYE4 brachydanto
39	65	33.9	52	4 Q8IXD5	Q8IXD5 homo sapien
40	64	33.3	678	4 Q14393	Q14393 homo sapien
41	63	32.8	52	4 Q8IXC5	Q8IXC5 homo sapien
42	63	32.8	673	11 Q61592	Q61592 mus musculu
43	63	32.8	674	11 Q99K57	Q99K57 mus musculu
44	62	32.3	226	11 Q8BX25	Q8BX25 mus musculu
45	62	32.3	226	11 Q8BGN6	Q8BGN6 mus musculu

## ALIGNMENTS

## RESULT 1

Q96P08 PRELIMINARY; PRT; 701 AA.  
ID Q96P08  
AC Q96P08  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Factor VII active site mutant immunocognate.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP  
SEQUENCE FROM N.A.  
RX MEDLINE=21477448; PubMed=11593034;  
RA Hu Z., Garen A.;  
RT "targeting tissue factor on tumor vascular endothelial cells and tumor  
cells for immunotherapy in mouse models of prostatic cancer."  
RT Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
DR EMBL: AF272774; AAKS8686.1; -.  
DR HSP, P00761; 1AN1.  
DR InterPro: IPR00152; Asx\_hydroxyl.  
DR InterPro: IPR001314; Chymotrypsin.  
DR InterPro: IPR000742; EGF 2.  
DR InterPro: IPR001881; EGF\_Ca.  
DR InterPro: IPR001438; EGF\_T1.  
DR InterPro: IPR006209; EGF\_like.  
DR InterPro: IPR002383; GLA\_blood.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003597; IG cl.  
DR InterPro: IPR003006; IG\_MHC.  
DR InterPro: IPR001254; Set\_protease\_Try.  
DR InterPro: IPR000294; VitK\_dep\_GLA.  
DR Pfam: PF00008; EGF 2.  
DR Pfam: PF00594; GLA 1.  
DR Pfam: PF00047; IG 1.  
DR Pfam: PF00089; trypsin 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00010; EGBLOOD.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00407; IGc1; 1.  
DR SMART; SM00020; TRYP\_Spc; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
DR PROSITE; PS00290; IG\_Mc; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW EGF-like domain; Hydrolase; Protease; Serine protease.  
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CB42C992F CRC64;

Query Match 64.1%; Score 123; DB 4; Length 701;  
Best Local Similarity 52.3%; Pred. No. 5.9e-14;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Oy 1 ANGFLXLRQSGSLKRCXKXLCSEFXAXHIFPNXXRTQFWVS 44  
Db 61 ANAFLEELRPSGLERCKEKECCSFEEAREIFKDAERTKLFWISY 104

## RESULT 2

Q8NEK6 PRELIMINARY; PRT; 268 AA.  
AC Q8NEK6;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Proline-rich Gla (G-carboxyglutamic acid) polypeptide 1  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RA Strausberg R.;  
RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.  
DR EMBL; BC030786; AAH30786.1; -;  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00594; gla; 1.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00069; GLA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
FT NON\_TER 1  
SQ SEQUENCE 268 AA; 30295 MW; C3A47C2D90007739 CRC64;

Query Match 58.9%; Score 113; DB 4; Length 268;  
Best Local Similarity 40.9%; Pred. No. 1.6e-12;  
Matches 18; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Oy 1 ANGFLXLRQSGSLKRCXKXLCSEFXAXHIFPNXXRTQFWVS 44  
Db 71 ANGFEELRQGNIERCKEKECTFEAREAREFENNEKTEKFWSTY 114

## RESULT 3

ID Q91WN8 PRELIMINARY; PRT; 460 AA.  
AC Q91WN8;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Similar to protein C.

GN PROC.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Strausberg R.;  
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.  
CC -1-SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

DR EMBL; BC013896; AAH13896.1; -.  
DR HSSP; P00761; IAN1.  
DR MGD; MGI:97771; Proc.  
DR InterPro; IPR000152; Asx\_hydroxyl.  
DR InterPro; IPR001314; Chymotrypsin.  
DR InterPro; IPR001881; EGF\_CA.  
DR InterPro; IPR006209; EGF\_Like.  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR001254; Ser\_protease\_Try.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00008; EGF; 2.

DR Pfam; PF00594; gla; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00001; GLABLOOD.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00069; GLA; 1.  
DR SMART; SM00020; TRYP\_Spc; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS00022; EGF\_2; 2.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS00011; GLU\_CARBOXYLATION; 1.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
KW EGF-like domain; Hydrolase; Protease; Serine protease.  
SQ SEQUENCE 460 AA; 51818 MW; 0117P26E8FCC274 CRC64;

Query Match 55.7%; Score 107; DB 11; Length 460;  
Best Local Similarity 45.5%; Pred. No. 3.6e-11;  
Matches 20; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Oy 1 ANGFLXLRQSGSLKRCXKXLCSEFXAXHIFPNXXRTQFWVS 44  
Db 42 ANSFLBEMRPSGLERCKEKEICDPEEAQEIFQNVEDTLFWIKY 85

## RESULT 4

Q8UJ40 PRELIMINARY; PRT; 229 AA.  
AC Q8UJ40;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Mitotic phosphoprotein 77 (Fragment).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxId=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21676254; PubMed=11818060;  
RA Georgi A.B., Stukenberg P.T., Kirschner M.W.;  
RT "Timing of events in mitosis."  
RL Curr. Biol. 12:105-114(2002).  
DR EMBL; AF419154; AAM3249.1; -;  
DR InterPro; IPR002383; GLA\_blood.  
DR InterPro; IPR000294; VitK\_dep\_GLA.  
DR Pfam; PF00594; gla; 1.  
DR PRINTS; PR00001; GLABLOOD.

DR SMART; 2500069; GLA; 1.  
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.  
 DR NCN TER 229  
 DR SEQUENCE 229 AA; 25543 MW; 42A2856BA6A9A9 CRC64;

Query Match 55.2%; Score 106; DB 13; Length 229;  
 Best Local Similarity 38.6%; Pred. No. 2.8e-11;  
 Matches 17; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

Qy 1 ANGFLLXLRGSLKRXCRXXLCSPXXAHXIFRNXXRTROFWVS 44  
 Db 21 ANSFLERIKQGNTERECKEELCTYEAREAFENDEKTEPWKEY 64

## RESULT 5

ID 061109 PRELIMINARY; PRT; 446 AA.  
 AC 061109;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Coagulation factor VII.  
 GN F7 OR FVII.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=96276538; PubMed=8701412;  
 RA Idusogie E., Rosen E., Geng J.P., Carmeliet P., Collen D.,  
 RA Castellino F.J.;  
 RT "Characterization of a cDNA encoding murine coagulation factor VII."  
 RL Thromb. Haemost. 75:481-487(1996).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 DR EMBL; U44795; AAC52570.1; -  
 DR HSSP; P08709; 1PAK.  
 DR MGD; MGI:109325; F7.  
 DR InterPro; IPR002086; Aldehyde dehydr.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR001064; Crystallin.  
 DR InterPro; IPR001881; EGF Ca.  
 DR InterPro; IPR006209; EGF\_Like.  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00008; EGF; 2.  
 DR Pfam; PF00594; gla; 1.  
 DR Pfam; PF00089; clypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00179; EGF CA; 1.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00020; TTP Src; 1.  
 DR PROSITE; PS00070; ALDEHYDE DEHYDR\_CYS; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00225; CRYSTALLIN\_BETAGAMMA; 1.  
 DR PROSITE; PS00022; EGF 1; 1.  
 DR PROSITE; PS01187; EGF CA; 1.  
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KM EGF-like domain; Hydroxylase; Protease; Serine protease.  
 SQ SEQUENCE 446 AA; 50318 MW; 482FD09BEFDA6870 CRC64;

Query Match 55.2%; Score 106; DB 11; Length 446;  
 Best Local Similarity 47.7%; Pred. No. 5.3e-11;  
 Matches 21; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLLXLRGSLKRXCRXXLCSPXXAHXIFRNXXRTROFWVS 44

Db 42 ANSLBELWPGSLERECNEQCSFEAREIFKSPERTKQFWIY 85

## RESULT 6

ID 06N2N6 PRELIMINARY; PRT; 231 AA.  
 AC 06N2N6;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Hypothetical protein FLJ90093.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RA Isegai T., Ota T., Nishikawa T., Hayaishi K., Otsuki T., Sugiyama T.,  
 RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,  
 RA Yamamoto J., Makamatsu A., Nakamura Y., Kojima S., Nagahara K.,  
 RA Masuno Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,  
 RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;  
 RT "NEDO human cDNA sequencing project."  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK074574; BA011069.1; -  
 DR InterPro; IPR002383; GLA\_blood.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00594; gla; 1.  
 DR PRINTS; PR00001; GLABLOOD.  
 DR SMART; SM00069; GLA; 1.  
 DR PROSITE; PS00011; GLU CARBOXYLATION; 1.  
 KM Hypothetical protein.  
 SQ SEQUENCE 231 AA; 25844 MW; 8A373B0D5C1D0D81 CRC64;

Query Match 54.7%; Score 105; DB 4; Length 231;  
 Best Local Similarity 40.9%; Pred. No. 4.2e-11;  
 Matches 18; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 1 ANGFLLXLRGSLKRXCRXXLCSPXXAHXIFRNXXRTROFWVS 44  
 Db 20 ANSFLERIKQGNTERECKEELCTYEAREAFENDEKTEPWKEY 63

## RESULT 7

ID 08JHC9 PRELIMINARY; PRT; 443 AA.  
 AC 08JHC9;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Coagulation factor VIII.  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hanumanthaiah R., Day K., Jagadeeswaran P.;  
 RT "Comprehensive analysis of blood coagulation pathways in Teleostei:  
 RT Evolution of coagulation factor genes and identification of zebrafish  
 RT factor VIII.";  
 RL Blood Cells Mol. Dis. 0:0-0(2002).  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 DR EMBL; AF519546; AA88342.1; -  
 DR EMBL; AF515269; AA871000.1; -  
 DR InterPro; IPR001314; Chymotrypsin.  
 DR InterPro; IPR000742; EGF 2.  
 DR InterPro; IPR001881; EGF Ca.  
 DR InterPro; IPR006209; EGF\_Like.  
 DR InterPro; IPR002383; GLA\_blood.

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DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00022; EGF_2; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR EGF-like domain; Hydrolase; Protease; Serine protease.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 443 AA; 48823 MW; 2D2504718AE9FF4 CRC64;

Query Match          54.7%; Score 105; DB 13; Length 443;
Best Local Similarity 39.5%; Pred. No. 8e-11;
Matches 17; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

Oy 2 NGFLXLRQGSILRXCRXXLCSPFXAHXIFRNXXRTROPWVS 44
Db 40 SGFLEMRKAGNLERCEVEICDYEAREVREDDRTKQFWLSY 82

RESULT 8
ID 099PC6 PRELIMINARY; PRT; 460 AA.
AC 099PC6
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Anticoagulant protein C.
OS PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Korf 1.;
RT "Complete sequence of UC72A01."
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AF318182; AAK07918.1; -.
DR HSSP; P04070; IAUT.
DR MGD; MGI:97771; Proc.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Ca.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR EGF-like domain; Hydrolase; Protease; Serine protease.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 446 AA; 50399 MW; 292985EBF119C0A4 CRC64;
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DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
DR EGF-like domain; Hydrolase; Protease; Serine protease.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 460 AA; 51784 MW; 0293BC259D3ED16 CRC64;

Query Match          52.6%; Score 101; DB 11; Length 460;
Best Local Similarity 43.2%; Pred. No. 4.6e-10;
Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

Oy 1 ANGFLXLRQGSILRXCRXXLCSPFXAHXIFRNXXRTROPWVS 44
Db 42 ANSFLEMRKAGNLERCEVEICDYEAREVREDDRTKQFWLSY 85

RESULT 9
ID 08K3U6 PRELIMINARY; PRT; 446 AA.
AC 08K3U6
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Coagulation factor VII.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Murphy K.; Ramaker M.;
RT "Nucleotide sequence of the cDNA encoding rat coagulation factor VII."
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AF532184; AAM95967.1; -.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_11.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Ser_protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF_2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 446 AA; 50399 MW; 292985EBF119C0A4 CRC64;

Query Match          51.0%; Score 98; DB 11; Length 446;
Best Local Similarity 45.5%; Pred. No. 1.6e-09;
Matches 20; Conservative 3; Mismatches 21; Indels 0; Gaps 0;

Oy 1 ANGFLXLRQGSILRXCRXXLCSPFXAHXIFRNXXRTROPWVS 44
Db 40 SGFLEMRKAGNLERCEVEICDYEAREVREDDRTKQFWLSY 82
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DB 42 ANSLBELMSSSLRECNBRCSEFEAREIFKSPERTKQWITY 85

RESULT 10

ID 097TRO PRELIMINARY; PRT; 456 AA.

AC 097TRO;

DT 01-MAY-2000 (T-EMBLrel. 13, Created)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)

DE Protein C precursor.

GN PROC.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI\_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RA Leeb T., Kopp T., Deppe A., Breen M., Mattis U., Brunberg L.,

RT "Molecular characterization and chromosomal assignment of the canine

RT protein C gene.";

RL Mamm. Genome 10:135-139(1999).

RN [2]

RX SEQUENCE FROM N.A.

RX MEDLINE=99371952; PubMed=10443005;

RA Leeb T., Pfeiffer I., Kopp T., Deppe A., Breenig B.,

RT "Analysis of canine protein C gene polymorphisms.";

RL Anim. Genet. 30:237-238(1999).

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

DR EMBL: AJ001979; CAA05126.1; -.

DR HSSP: P04070; 1AUT.

DR InterPro: IPR000152; Asx\_hydroxyl.

DR InterPro: IPR001314; Chymotrypsin.

DR InterPro: IPR001881; EGF\_Ca.

DR InterPro: IPR006209; EGF\_like.

DR InterPro: IPR002383; GLA\_blood.

DR InterPro: IPR006210; IEGF.

DR InterPro: IPR001254; Ser\_protease\_Try.

DR InterPro: IPR000294; VitK\_dep\_GLA.

DR Pfam: PF00008; EGF\_2.

DR Pfam: PF00594; GLA; 1.

DR Pfam: PF00089; trypsin; 1.

DR PRINTS: PR00722; CHYMOTRYPSIN.

DR PRINTS: PR00001; GLABLOOD.

DR SMART: SM00181; EGF; 2.

DR SMART: SM00069; GLA; 1.

DR SMART: SM00020; TRYF\_SPC; 1.

DR PROSITE: PS00010; ASX\_HYDROXYL; 1.

DR PROSITE: PS00022; EGF\_1; 1.

DR PROSITE: PS01186; EGF\_2; 2.

DR PROSITE: PS01187; EGF\_CA; 1.

DR PROSITE: PS00011; GLU CARBOXYLATION; 1.

DR PROSITE: PS00240; TRYPsin DOM; 1.

DR PROSITE: PS00134; TRYPsin\_HIS; 1.

DR PROSITE: PS00135; TRYPsin\_SER; 1.

KW EGF-like domain; Hydroxylase; Protease; Serine protease; Signal.

FT STGNLV 1 42 POTENTIAL.

FT CHAIN 1 192 PROTEIN C LIGHT CHAIN.

FT CHAIN 193 194 PROTEIN C CONNECTING DIPEPTIDE.

FT CHAIN 195 456 PROTEIN C HEAVY CHAIN.

SQ SEQUENCE 456 AA; 50813 MW; 7AD3A8C1C34E59FF CRC64;

Query Match 51.0%; Score 98; DB 6; Length 456;

Best Local Similarity 43.2%; Pred. No. 1.6e-09;

Matches 19; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 1 ANGFLXXRQSLXRXCRXXLCSFYXAHXIFRNXXRTROFWVSY 44

DB 43 ANSFLEIRAGSLERECMEIEICDEEAKELFQNDVDTLAYWSKY 86

RESULT 11

063207

ID 063207 PRELIMINARY; PRT; 482 AA.

AC 063207;

DT 01-NOV-1996 (T-EMBLrel. 01, Created)

DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)

DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)

DE Factor X.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;

RX MEDLINE=96083366; PubMed=8578539;

RA Stanton C., Ross R.P., Hutson S., Wallin R.,

RT "Evidence for competition between vitamin K-dependent clotting factors

RT for intracellular processing by the vitamin K-dependent gamma-

RT carboxylase.";

RL Thromb. Res. 80:63-73(1995).

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

DR EMBL: X79807; CAA56202.1; -.

DR HSSP: P00742; 1XKA.

DR MEROPS: S01.216; -.

DR InterPro: IPR000152; Asx\_hydroxyl.

DR InterPro: IPR001314; Chymotrypsin.

DR InterPro: IPR000742; EGF\_2.

DR InterPro: IPR001881; EGF\_Ca.

DR InterPro: IPR001438; EGF\_1I.

DR InterPro: IPR006209; EGF\_like.

DR InterPro: IPR002383; GLA\_blood.

DR InterPro: IPR001254; Ser\_protease\_Try.

DR InterPro: IPR000294; VitK\_dep\_GLA.

DR Pfam: PF00008; EGF; 2.

DR Pfam: PF00594; GLA; 1.

DR Pfam: PF00089; trypsin; 1.

DR PRINTS: PR00722; CHYMOTRYPSIN.

DR PRINTS: PR00010; GLABLOOD.

DR PRINTS: PR00001; GLABLOOD.

DR SMART: SM00179; EGF\_CA; 1.

DR SMART: SM00069; GLA; 1.

DR SMART: SM00020; TRYF\_SPC; 1.

DR PROSITE: PS00010; ASX\_HYDROXYL; 1.

DR PROSITE: PS00022; EGF\_1; 1.

DR PROSITE: PS01186; EGF\_2; 2.

DR PROSITE: PS01187; EGF\_CA; 1.

DR PROSITE: PS00011; GLU CARBOXYLATION; 1.

DR PROSITE: PS00240; TRYPsin DOM; 1.

DR PROSITE: PS00134; TRYPsin\_HIS; 1.

DR PROSITE: PS00135; TRYPsin\_SER; 1.

KW EGF-like domain; Hydroxylase; Protease; Serine protease.

SQ SEQUENCE 482 AA; 54265 MW; 0284678E3954A698 CRC64;

Query Match 50.0%; Score 96; DB 11; Length 482;

Best Local Similarity 36.4%; Pred. No. 4e-09;

Matches 16; Conservative 9; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXRQSLXRXCRXXLCSFYXAHXIFRNXXRTROFWVSY 44

DB 41 ANSFEEIKGNLRECVBEICSEFEAREVFEEDNEKTEFFMNXY 84

RESULT 12

ID 014316

AC 014316 PRELIMINARY; PRT; 456 AA.

DT 01-NOV-1996 (T-EMBLrel. 01, Created)

DT 01-ANG-1999 (T-EMBLrel. 11, Last sequence update)

DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)

DE F9 (Coagulation factor IX (Plasma THROMBOPLASTIC component, christmas

DE disease, HAEMOPHILIA B)) (Factor IX).

GN F9 OR FACTOR IX.

OS Homo sapiens (human).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 3-19 FROM N.A.
RX MEDLINE=88327116; PubMed=3416069;
RA Beltman P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,
RA Bret E.;
RT "The putative factor IX gene promoter in hemophilia B Leyden.";
RL Blood 72:1074-1076(1988).
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AL033403; CAA21954.1; -.
DR EMBL; X55008; CAB38245.2; -.
DR HSSP; P00740; ICPH.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF_IT.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF000594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBLD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 456 AA; 51149 MW; 54E20A1B3964E234 CRC64;

Query Match 48.4%; Score 93; DB 4; Length 456;
Best Local Similarity 41.9%; Pred. No. 1.4e-08;
Matches 18; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

OY 2 NGFLXLRQGSILRXCRXLCSPFXAHXIFRNXXRTQFWVSY 44
Db 44 SGKLEFVQGNLERECMEKCSFEAREVFENTERITTEFWKQY 86

RESULT 13
O95ND7 PRELIMINARY; PRT; 461 AA.
AC O95ND7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=504;
RA Sacta Y.;

```

```

RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RL Genes Genet. Syst. 0:0-0(2001).
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB062470; BAB58885.1; JOINED.
DR EMBL; AB062458; BAB58885.1; JOINED.
DR EMBL; AB062460; BAB58885.1; JOINED.
DR EMBL; AB062462; BAB58885.1; JOINED.
DR EMBL; AB062464; BAB58885.1; JOINED.
DR EMBL; AB062466; BAB58885.1; JOINED.
DR EMBL; AB062468; BAB58885.1; JOINED.
DR HSSP; P00761; IAN1.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF_IT.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF000594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGFBLD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Hydrolase; Protease; Serine protease.
SQ SEQUENCE 461 AA; 51764 MW; 30C2F857C0F77F45 CRC64;

Query Match 48.4%; Score 93; DB 6; Length 461;
Best Local Similarity 41.9%; Pred. No. 1.4e-08;
Matches 18; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

OY 2 NGFLXLRQGSILRXCRXLCSPFXAHXIFRNXXRTQFWVSY 44
Db 49 SGKLEFVQGNLERECMEKCSFEAREVFENTERITTEFWKQY 91

RESULT 14
O95ND6 PRELIMINARY; PRT; 461 AA.
AC O95ND6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Coagulation factor XI.
GN F9.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=505;
RA Sacta Y.;
RT "Comparison of DNA and protein polymorphisms between humans and
RT chimpanzees.";
RL Genes Genet. Syst. 0:0-0(2001).
CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB062471; BAB58886.1; JOINED.

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DR EMBL; AB062461; BAB58886.1; JOINED.
DR EMBL; AB062463; BAB58886.1; JOINED.
DR EMBL; AB062465; BAB58886.1; JOINED.
DR EMBL; AB062467; BAB58886.1; JOINED.
DR EMBL; AB062469; BAB58886.1; JOINED.
DR HSSP; P00761; IAN1.
DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_III.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; GLABLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRY_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00022; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS01187; EGF_II; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
DR EGF-like domain; Hydrolase; Protease; Serine protease.
DR SEQUENCE 461 AA; 51695 MW; 8F5A69A525DF6585 CRC64;

Query Match 48.4%; Score 93; DB 6; Length 461;
Best Local Similarity 41.9%; Pred. No. 1.4e-08;
Matches 18; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

OY 2 NGFLKXLRQGSLLKRCXKXLCSEFYXAHXIFRNXXRTPOFWVS 44
Db 49 SGKLEBFVQGNLRECEMEKCSFEAREVFEFTEFTEFWKQY 91

RESULT 15
O54740 PRELIMINARY; PRT; 481 AA.
AC O54740;
DT 01-JUN-1998 (Tremblere1.06, Created)
DT 01-JUN-1998 (Tremblere1.06, Last sequence update)
DT 01-MAR-2003 (Tremblere1.23, Last annotation update)
DE Coagulation factor X precursor (EC 3.4.21.6).
GN F10 OR F10.
OS Mus musculus (Mouse).
OC Plasmid BLUEScript.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxonomy10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98454993; PubMed=9783672;
RA Heidemann H.H., Kontermann R.E.;
RT "Cloning and recombinant expression of mouse coagulation factor X.";
RL Thromb. Res. 92:33-41(1998).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AJ222677; CAA10933.1; -.
DR HSSP; P00742; IKKA.
DR MEROPS; S01.216; -.
DR MGD; MGI:103107; F10.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000742; EGF_2.
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DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_III.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001254; Ser protease_Try.
DR InterPro; IPR000294; VltK_dep_GLA.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; GLABLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00020; TRY_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00022; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE; PS00240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
DR EGF-like domain; Hydrolase; Protease; Serine protease; Signal;
KW Plasmid.
FT SIGNAL 1 40
FT CHAIN 41 481 COAGULATION FACTOR X.
SQ SEQUENCE 481 AA; 53986 MW; CF702DESEF9D97AE CRC64;

Query Match 48.4%; Score 93; DB 11; Length 481;
Best Local Similarity 31.8%; Pred. No. 1.4e-08;
Matches 14; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

OY 1 ANGLKXLRQGSLLKRCXKXLCSEFYXAHXIFRNXXRTPOFWVS 44
Db 41 ANSFFBFFKXGNLRECEMEKCSFEAREVFEFTEFTEFWKQY 84

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 28, 2003, 12:11:15 ; Search time 37 Seconds  
(without alignments)  
188.756 Million cell updates/sec

Title: SEQ4  
Perfect score: 192  
Sequence: 1 ANGELXXLRGSLXRCRX.....XXAHXIPRNXXRQFWVSY 44

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqe, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164	85.4	44	AA18306	Bovine factor VII
2	164	85.4	44	AA18306	Bovine factor VII
3	127	66.1	44	AA18302	Modified GLA domain
4	126	65.6	44	AA18310	Modified GLA domain
5	124	64.6	44	AA18311	Modified GLA domain
6	123	64.1	44	AA18305	Human factor VII G
7	123	64.1	44	AA18305	Human factor VII G
8	123	64.1	401	AA184870	Mutant blood coagu
9	123	64.1	401	AA184871	Mutant blood coagu

10	123	64.1	406	AA183764	Factor VII (VII) .
11	123	64.1	406	AA184509	Modified blood coa
12	123	64.1	406	AA184510	Modified blood coa
13	123	64.1	406	AA184510	Modified blood coa
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15	123	64.1	406	AA184510	Modified blood coa
16	123	64.1	406	AA184510	Modified blood coa
17	123	64.1	406	AA184510	Modified blood coa
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45	123	64.1	406	AA184510	Modified blood coa

#### ALIGNMENTS

RESULT 1	
ID	AA18306
AA18306	standard; peptide; 44 AA.
XX	AA18306;
AC	AA18306;
XX	17-AUG-1999 (first entry)
DT	17-AUG-1999 (first entry)
XX	Bovine factor VII GLA domain.
XX	Bovine factor VII GLA domain.
KW	GLA domain; vitamin K-dependent protein; clotting disorder;
KM	therapy.
XX	
OS	Bos taurus.
XX	
FH	Key
FT	Misc-difference 1..44
FT	/note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
XX	
PN	MO9920767-A1.
XX	
PD	29-APR-1999.
XX	
PF	20-OCT-1998; 98MO-US22152.
XX	
PR	23-OCT-1997; 97US-0955636.
XX	
PA	(MINU ) UNIV MINNESOTA.
XX	
PI	Neisectuen GL;
XX	

DR WPI: 1999-288309/24.

XX

PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic

PT acid domain, useful for treating clotting disorders

XX

PS Disclosure; Page 15; 86pp; English.

XX

CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)

CC domain. The invention relates to a vitamin K-dependent polypeptide

CC comprising a modified GLA domain containing an amino acid substitution

CC which enhances membrane binding of the modified polypeptide as compared

CC to the native polypeptide. The polypeptide is used to treat a clotting

CC disorder by decreasing or increasing clot formation. Modification of the

CC GLA domain results in a protein which has enhanced membrane binding

CC affinity as compared to the native protein.

XX

XX Sequence 44 AA:

SO

Query Match 85.4%; Score 164; DB 20; Length 44;

Best Local Similarity 97.7%; Pred. No. 4.5e-21;

Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRQSLXRCXKXLCSPFXAXHIFRNXXRTQFWVS 44

Db 1 ANGFLXXLRQSLXRCXKXLCSPFXAXHIFRNXXRTQFWVS 44

RESULT 2

AAB36396

ID AAB36396 standard; peptide; 44 AA.

XX

AC AAB36396;

XX

DT 27-FEB-2001 (first entry)

XX

XX Bovine factor VII gamma-carboxyglutamic acid domain SEQ ID NO:4.

DE

XX

XX Vitamin K-dependent protein; factor VII; protein C; GLA domain;

KM gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;

KM factor X; prothrombin; enhanced membrane binding affinity;

KM clot formation; thrombolytic; haemostatic; bleeding disorder;

KM thrombosis; clotting disorder; haemophilia A; haemophilia B;

KM liver disease.

XX

OS Bos taurus.

XX

XX WO20006753-A2.

XX

XX 09-NOV-2000.

PD

XX

XX 28-APR-2000; 2000WO-US11416.

PF

XX

XX 29-APR-1999; 99US-0302239.

PR

XX

XX (MINU ) UNIV MINNESOTA.

PA

XX

PI Neiseetuen GL;

PI

XX

XX WPI: 2001-007226/01.

DR

XX

XX Novel vitamin K-dependent polypeptide useful for treating clotting

PT disorders such as thrombosis and hemophilia, comprising modified

PT gamma-carboxy glutamic acid domain that enhances membrane binding

PT affinity -

XX

XX Disclosure; Page 12; 81pp; English.

XX

XX The present invention describes a vitamin K-dependent polypeptide (I)

CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having

CC at least one amino acid substitution, that enhances membrane binding

CC affinity and the activity of the polypeptide relative to a corresponding

CC native vitamin K-dependent polypeptide and inhibits clot formation.

CC (I) can have thrombolytic and haemostatic activities, and can be used

CC as an inhibitor of clot formation. (I) is useful for decreasing clot

CC formation in a mammal, a factor VII or factor IX containing a modified

CC GLA domain is useful for increasing clot formation and for treating a

CC bleeding disorder, including thrombosis and clotting disorders such as

CC haemophilia A, haemophilia B and liver disease. The present sequence

CC represents a wild type bovine factor VII GLA domain sequence, given in

CC the exemplification of the present invention.

XX

XX Sequence 44 AA:

SO

Query Match 85.4%; Score 164; DB 22; Length 44;

Best Local Similarity 97.7%; Pred. No. 4.5e-21;

Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ANGFLXXLRQSLXRCXKXLCSPFXAXHIFRNXXRTQFWVS 44

Db 1 ANGFLXXLRQSLXRCXKXLCSPFXAXHIFRNXXRTQFWVS 44

RESULT 3

AAV18302

ID AAV18302 standard; peptide; 44 AA.

XX

AC AAV18302;

XX

DT 17-AUG-1999 (first entry)

XX

XX Modified GLA domain of vitamin K-dependent protein.

DE

XX

XX GLA domain; mutein; vitamin K-dependent protein; clotting disorder;

KM therapy.

KM

XX

XX Homo sapiens.

OS

XX

XX Synthetic.

OS

XX

XX Key Location/Qualifiers

FM Misc-difference 1..44

FT "Xaa" gamma-carboxyglutamic acid, or glutamic

FT acid"

XX

XX WO9920767-A1.

XX

XX 29-APR-1999.

PD

XX

XX 20-OCT-1998; 98WO-US22152.

PF

XX

XX 23-OCT-1997; 97US-0955636.

PR

XX

XX (MINU ) UNIV MINNESOTA.

PA

XX

PI Neiseetuen GL;

PI

XX

XX WPI: 1999-288309/24.

DR

XX

XX Claim 11; Page 81; 86pp; English.

XX

XX This sequence represents a modified GLA (gamma-carboxyglutamic acid)

CC domain. The invention relates to a vitamin K-dependent polypeptide

CC comprising a modified GLA domain containing an amino acid substitution

CC which enhances membrane binding of the modified polypeptide as compared

CC to the native polypeptide. The polypeptide is used to treat a clotting

CC disorder by decreasing or increasing clot formation. Modification of the

CC GLA domain results in a protein which has enhanced membrane binding

CC affinity as compared to the native protein.

XX

XX Sequence 44 AA:

SO

Query Match 66.1%; Score 127; DB 20; Length 44;

Best Local Similarity 77.3%; Pred. No. 1.3e-14;

Matches 34; Conservative 4; Mismatches 6; Indels 0; Gaps 0;



PM WO9920767-A1.  
XX  
PD 29-APR-1999.  
XX  
PF 20-OCT-1998; 98WO-US22152.  
XX  
PR 23-OCT-1997; 97US-0955636.  
XX  
PA (MINU ) UNIV MINNESOTA.  
XX  
PI Nelsestuen GL;  
XX  
DR WPI; 1999-288309/24.  
XX  
PT Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic  
XX acid domain, useful for treating clotting disorders  
XX  
PS Disclosure; Page 15; 86pp; English.  
XX  
CC This sequence is the factor VII GLA (gamma-carboxyglutamic acid)  
CC domain. The invention relates to a vitamin K-dependent polypeptide  
CC comprising a modified GLA domain containing an amino acid substitution  
CC which enhances membrane binding of the modified polypeptide as compared  
CC to the native polypeptide. The polypeptide is used to treat a clotting  
CC disorder by decreasing or increasing clot formation. Modification of the  
CC GLA domain results in a protein which has enhanced membrane binding  
CC affinity as compared to the native protein.  
XX  
SQ Sequence 44 AA;  
XX  
Query Match 64.1%; Score 123; DB 20; Length 44;  
Best Local Similarity 75.0%; Pred. No. 6.4e-14;  
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
Oy 1 ANGFLXXLRQGLXRXCRXXLCSFXXAHXIFRNXXRTQFWVSX 44  
1 ANAFXXLRPGSLXRXCKXXCSPXXAXRIFDXAXRTLFWISY 44  
Db  
RESULT 7  
AAB36395  
ID AAB36395 standard; peptide; 44 AA.  
XX  
AC AAB36395;  
XX  
DT 27-FEB-2001 (first entry)  
XX  
DE Human factor VII gamma-carboxyglutamic acid domain SEQ ID NO:3.  
XX  
KW Vitamin K-dependent protein; factor VII; protein C; GLA domain;  
KW gamma-carboxyglutamic acid domain; factor IX; protein S; protein Z;  
KW factor X; prothrombin; enhanced membrane binding affinity;  
KW clot formation; thrombolytic; haemostatic; bleeding disorder;  
KW thrombosis; clotting disorder; haemophilia A; haemophilia B;  
KW liver disease.  
XX  
OS Homo sapiens.  
XX  
PN MO20006753-A2.  
XX  
PD 09-NOV-2000.  
XX  
PF 28-APR-2000; 2000WO-US11416.  
XX  
PR 29-APR-1999; 99US-0302239.  
XX  
PA (MINU ) UNIV MINNESOTA.  
XX  
PI Nelsestuen GL;  
XX  
DR WPI; 2001-007226/01.  
XX  
PT Novel vitamin K-dependent polypeptide useful for treating clotting

PT disorders such as thrombosis and hemophilia, comprises modified  
PT gamma-carboxy glutamic acid domain that enhances membrane binding  
PT affinity -  
XX  
PS Disclosure; Page 12; 81pp; English.  
XX  
CC The present invention describes a vitamin K-dependent polypeptide (I)  
CC comprising a modified gamma-carboxy glutamic acid (GLA) domain having  
CC at least one amino acid substitution, that enhances membrane binding  
CC affinity and the activity of the polypeptide relative to a corresponding  
CC native vitamin K-dependent polypeptide and inhibits clot formation.  
CC (I) can have thrombolytic and haemostatic activities, and can be used  
CC as an inhibitor of clot formation. (I) is useful for decreasing clot  
CC formation in a mammal, a factor VII or factor IX containing a modified  
CC GLA domain is useful for increasing clot formation and for treating a  
CC bleeding disorder, including thrombosis and clotting disorders such as  
CC haemophilia A, haemophilia B and liver disease. The present sequence  
CC represents a wild type human factor VII GLA domain sequence, given in  
CC the exemplification of the present invention.  
XX  
SQ Sequence 44 AA;  
XX  
Query Match 64.1%; Score 123; DB 22; Length 44;  
Best Local Similarity 75.0%; Pred. No. 6.4e-14;  
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;  
Oy 1 ANGFLXXLRQGLXRXCRXXLCSFXXAHXIFRNXXRTQFWVSX 44  
1 ANAFXXLRPGSLXRXCKXXCSPXXAXRIFDXAXRTLFWISY 44  
Db  
RESULT 8  
AAB84870  
ID AAB84870 standard; Protein; 401 AA.  
XX  
AC AAB84870;  
XX  
DT 31-JUL-2001 (first entry)  
XX  
DE Mutant blood coagulant factor VII (FVII-31).  
XX  
KW Human; haemostatic; blood coagulant factor VII; FVII; haemophilia;  
KW mutant; mutcin.  
XX  
OS Homo sapiens.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 311..317  
FT /note= "Wild-type Leu-Gln-Gln-Ser-Arg-Lys-Val-Gly-Asp  
FT -Ser-Pro-Asn substituted by Gln-Ala-Ser-Tyr-Pro-Gly-Lys"  
XX  
XX JP2001061479-A.  
PD 13-MAR-2001.  
XX  
XX 24-AUG-1999; 99JP-0237610.  
XX  
XX 24-AUG-1999; 99JP-0237610.  
XX  
PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.  
XX  
XX WPI; 2001-310677/33.  
DR N-PSDB; AAH19463.  
XX  
PT Mutant of blood coagulant factor VII, used for substitution therapy in  
PT the treatment of hemophilia -  
XX  
PS Claim 14; Page 20-21; 29pp; Japanese.  
XX  
CC The present invention relates to mutants of blood coagulant factor VII  
CC (FVII) or activated blood coagulant factor VII (FVIIa). The present  
CC sequence is one such mutant FVII: VII-31. The mutants can be used as an



[illegible][illegible]



```
XX AC AAU77745;
XX DT 05-JUN-2002 (first entry)
XX DE Human factor VIIa active site mutant.
XX KM Factor VIIa; human; shock heat treatment; protein stability;
XX KW protein manufacture; protein conformation; mutant; mutein.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FH FT Active-site 193
FT FT Active-site /note= "Member of the factor VIIa catalytic triad"
FT FT Active-site 242
FT FT Active-site /note= "Member of the factor VIIa catalytic triad"
FT FT Active-site 344
FT FT Active-site /note= "Member of the factor VIIa catalytic triad"
FT FT Misc-difference 344
FT FT /label= Gly, Met, Thr
FT FT /note= "Preferably Ala. Wild type Ser"
XX FT
XX FN WO200177141-A1.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-DK00234.
XX PR 06-APR-2000; 2000DK-0000573.
XX PR 17-APR-2000; 2000US-197650P.
XX PA (NOVO ) NOVO NORDISK AS.
XX PI Mathiesen F;
XX DR WPI; 2001-657162/75.
XX PT Stabilisation of a polypeptide e.g. in a pharmaceutical composition
XX PT involves a shock heat treatment.
XX PS Disclosure; Page -: 22pp; English.
XX CC The invention describes a method of stabilising a polypeptide involving
CC shock heat treatment of the polypeptide. The method is useful in a
CC pharmaceutical composition, in the industrial or large scale method of
CC manufacturing a polypeptide, also as a unit operation during preparation,
CC purification, recovery and/or formulation of polypeptides. The shock heat
CC treatment improves the protein stability without substantial loss of
CC biological activity. The method can be applied to change polypeptide
CC conformation in a very fast and non-invasive manner. The polypeptide
CC formed is stable. The method is also useful for decreasing the
CC association of the polypeptide. This sequence represents a modified
CC human factor VIIa protein, mutated at the catalytic site, described
CC in the invention.
CC Note: This sequence does not appear in the specification but has
CC been obtained using information given in the invention.
XX SQ Sequence 406 AA;

Query Match 64.1%; Score 123; DB 22; Length 406;
Best Local Similarity 52.3%; Pred. No. 6e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRQSGLXRCXRXLCSEFXAXHIFPNXXRTQFWVSY 44
Db 1 ANAFLELRPGSLERCKEBCQCSFEAREIFDQARTKLFWISY 44
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XX AC AAM52171;
XX DT 07-FEB-2002 (first entry)
XX DE Human FVII SEQ ID NO 1.
XX KM Factor VII; FVII; Factor VIIa; haemostatic; thrombolytic;
XX KW cardiatic; hepatocrophic; cerebroprotective; haemophilia; liver disease;
XX KW myocardial infarction; thrombotic stroke; deep-vein thrombosis.
XX OS Homo sapiens.
XX OS
XX FH Key Location/Qualifiers
FH FT Misc-difference 6
FT FT /label= Glu, OTHER
FT FT /note= "OTHER = gamma carboxyglutamic acid"
FT FT Misc-difference 7
FT FT /label= Glu, OTHER
FT FT /note= "OTHER = gamma carboxyglutamic acid"
FT FT Misc-difference 14
FT FT /label= Glu, OTHER
FT FT /note= "OTHER = gamma carboxyglutamic acid"
FT FT Misc-difference 16
FT FT /label= Glu, OTHER
FT FT /note= "OTHER = gamma carboxyglutamic acid"
FT FT Misc-difference 19
FT FT /label= Glu, OTHER
FT FT /note= "OTHER = gamma carboxyglutamic acid"
FT FT Misc-difference 20
FT FT /label= Glu, OTHER
FT FT /note= "OTHER = gamma carboxyglutamic acid"
FT FT Misc-difference 25
FT FT /label= Glu, OTHER
FT FT /note= "OTHER = gamma carboxyglutamic acid"
FT FT Misc-difference 26
FT FT /label= Glu, OTHER
FT FT /note= "OTHER = gamma carboxyglutamic acid"
FT FT Misc-difference 29
FT FT /label= Glu, OTHER
FT FT /note= "OTHER = gamma carboxyglutamic acid"
FT FT Misc-difference 35
FT FT /label= Glu, OTHER
FT FT /note= "OTHER = gamma carboxyglutamic acid"
FT FT Modified-site 52
FT FT /note= "O-glycosylated"
FT FT Modified-site 60
FT FT /note= "O-glycosylated"
FT FT Modified-site 145
FT FT /note= "N-glycosylated"
FT FT Cleavage-site 152..153
FT FT /note= "proteolytic cleavage site converting FVII zymogen
FT FT to an activated form, comprising two chains
FT FT linked by a single disulphide bridge"
FT FT Modified-site 322
FT FT /note= "N-glycosylated"
XX FT
XX FN WO200158935-A2.
XX PD 16-AUG-2001.
XX PF 12-FEB-2001; 2001WO-DK00094.
XX PR 11-FEB-2000; 2000DK-0000218.
XX PR 18-OCT-2000; 2000DK-0001558.
XX PA (MAXY-) MAXYGEN APS.
XX PI Andersen KV, Pedersen AH, Bornaes C;
XX DR WPI; 2001-581807/65.
XX DR N-PSDB; AAI99982.
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OM protein - protein search, using sw model

Run on: July 28, 2003, 12:25:31 ; Search time 32.5 Seconds

(without alignments)  
160.782 Million cell updates/sec

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Perfect score: 122  
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Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA:\*

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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
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9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
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12: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164	85.4	44	US-10-298-330-4	Sequence 4, Appl1
2	123	64.1	44	US-10-298-330-3	Sequence 3, Appl1
3	123	64.1	406	US-09-782-5878-1	Sequence 1, Appl1
4	123	64.1	406	US-09-782-5878-3	Sequence 3, Appl1
5	123	64.1	406	US-10-109-498-1	Sequence 1, Appl1
6	123	64.1	406	US-10-255-032-1	Sequence 1, Appl1
7	123	64.1	406	US-10-281-727-1	Sequence 1, Appl1
8	123	64.1	466	US-10-017-122-2	Sequence 2, Appl1
9	104	54.2	40	US-10-298-330-23	Sequence 2, Appl1
10	102	53.1	40	US-10-298-330-26	Sequence 26, Appl1
11	101	52.6	40	US-10-298-330-25	Sequence 25, Appl1
12	98	51.0	40	US-10-298-330-22	Sequence 22, Appl1
13	97	50.5	44	US-10-298-330-2	Sequence 2, Appl1
14	96	50.0	419	US-10-182-263-6	Sequence 6, Appl1
15	95	49.5	40	US-10-298-330-24	Sequence 24, Appl1

16	93	48.4	415	9	US-09-118-748-2	Sequence 2, Appl1
17	93	48.4	461	9	US-09-884-901-3	Sequence 3, Appl1
18	93	48.4	461	15	US-10-132-829-5	Sequence 5, Appl1
19	93	48.4	461	15	US-10-234-406-6	Sequence 6, Appl1
20	93	48.4	461	15	US-10-234-406-8	Sequence 8, Appl1
21	91	47.4	44	15	US-10-298-330-18	Sequence 18, Appl1
22	91	47.4	44	15	US-10-298-330-18	Sequence 18, Appl1
23	91	47.4	419	15	US-09-978-917A-4	Sequence 4, Appl1
24	91	47.4	419	15	US-10-182-263-1	Sequence 1, Appl1
25	91	47.4	419	15	US-10-182-263-3	Sequence 3, Appl1
26	91	47.4	419	15	US-10-182-263-4	Sequence 4, Appl1
27	91	47.4	419	15	US-10-182-263-5	Sequence 5, Appl1
28	91	47.4	461	11	US-09-978-917A-2	Sequence 2, Appl1
29	91	47.4	461	15	US-10-182-263-2	Sequence 2, Appl1
30	89	46.4	45	15	US-10-298-330-5	Sequence 5, Appl1
31	86	44.8	41	15	US-10-298-330-27	Sequence 27, Appl1
32	80	41.7	622	15	US-10-020-141-8	Sequence 8, Appl1
33	80	41.7	622	15	US-10-017-631-2	Sequence 2, Appl1
34	80	41.7	622	15	US-10-214-932-116	Sequence 116, App
35	80	41.7	622	15	US-10-172-712-29	Sequence 29, Appl1
36	78.5	40.9	46	15	US-10-298-330-6	Sequence 6, Appl1
37	73	38.0	44	15	US-10-298-330-19	Sequence 19, Appl1
38	70	36.5	45	15	US-10-298-330-17	Sequence 17, Appl1
39	70	36.5	96	11	US-09-759-130B-313	Sequence 13, App
40	70	36.5	96	15	US-10-189-123-43	Sequence 43, Appl1
41	70	36.5	209	11	US-09-759-130B-312	Sequence 312, App
42	70	36.5	209	15	US-10-189-123-42	Sequence 42, Appl1
43	70	36.5	226	11	US-09-759-130B-310	Sequence 310, App
44	70	36.5	226	15	US-10-189-123-40	Sequence 40, Appl1
45	63	32.8	673	15	US-10-223-085-48	Sequence 48, Appl1

## ALIGNMENTS

RESULT 1  
US-10-298-330-4  
; Sequence 4, Application US/10298330  
; Publication No. US20030100506A1  
; GENERAL INFORMATION:  
; APPLICANT: Neleestuen, Gary L.  
; TITLE OF INVENTION: Modified Vitamin K-Dependent  
; FILE REFERENCE: 09531-127001  
; CURRENT APPLICATION NUMBER: US/10/298,330  
; PRIOR FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/497,591  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/302,239  
; PRIOR FILING DATE: 1999-04-29  
; PRIOR APPLICATION NUMBER: 08/955,636  
; PRIOR FILING DATE: 1997-10-23  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 44  
; TYPE: PRT  
; ORGANISM: Bos taurus  
; FEATURES:  
; NAME/KEY: VARIANT  
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 34, 35  
; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid or glutamic acid  
US-10-298-330-4

Query Match 85.4%; Score 164; DB 15; Length 44;  
Best Local Similarity 97.7%; Pred. No. 4.2e-21;  
Matches 43; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 ANGFLXXLRQSLXRCRX...XXAHXIFRNXXRTQFWVSY 44  
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RESULT 2
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; Sequence 3, Application US/10298330
; Publication No. US20030100506A1
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary L.
; TITLE OF INVENTION: Modified Vitamin K-Dependent
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 09531-127001
; CURRENT APPLICATION NUMBER: US/10/298,330
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/497,591
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/302,239
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 08/955,636
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 35
; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid or glutamic acid
US-10-298-330-3

Query Match          64.1%; Score 123; DB 15; Length 44;
Best Local Similarity 75.0%; Pred. No. 5e-14;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 ANGFLXLRQGSILKRXCRXXLCSPFXAXHIFRNXXRTQFVWSY 44
DB 1 ANAFLLXLRPGSLKRXCKXQCSFXXARXIFKDXARTLFWISY 44

RESULT 3
US-09-782-587B-1
; Sequence 1, Application US/09782587B
; Publication No. US20030096338A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: BORNAES, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
; PRIOR FILING DATE: 2000-10-18
; NUMBER OF SEQ ID NOS: 19
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; ORGANISM: Homo sapiens
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; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
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; LOCATION: (16)
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; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
US-09-782-587B-1

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Best Local Similarity 75.0%; Pred. No. 4e-13;
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DB 1 ANAFLEELRPGSLERCKEQCSFEAREIFKDXARTLFWISY 44

RESULT 4
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; Sequence 3, Application US/09782587B
; Publication No. US20030096338A1
; GENERAL INFORMATION:
; APPLICANT: PEDERSEN, ANDERS H.
; APPLICANT: BORNAES, CLAUS
; TITLE OF INVENTION: FACTOR VII OR VIIA-LIKE MOLECULES
; FILE REFERENCE: 31-001100US
; CURRENT APPLICATION NUMBER: US/09/782,587B
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: PA 2000 00218
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,036
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/241,916
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; LENGTH: 406
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; ORGANISM: Homo sapiens
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; LOCATION: (6)..(7)
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; NAME/KEY: MOD_RES
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; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
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; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
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; LOCATION: (25)..(26)
; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
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; OTHER INFORMATION: Gamma carboxyglutamic acid or glutamic acid
US-09-782-587B-3

Query Match          64.1%; Score 123; DB 11; Length 406;
Best Local Similarity 52.3%; Pred. No. 4e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRQGSILKRXCRXXLCSPFXAXHIFRNXXRTQFVWSY 44
DB 1 ANAFLEELRPGSLERCKEQCSFEAREIFKDXARTLFWISY 44

RESULT 5
US-10-109-498-1
; Sequence 1, Application US/10109498
; Publication No. US20030044908A1
; GENERAL INFORMATION:
; APPLICANT: Persson, Egon
; TITLE OF INVENTION: Coagulation Factor VII Derivatives
; FILE REFERENCE: 6286 200-US
; CURRENT APPLICATION NUMBER: US/10/109,498
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 60/281,261
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: PA 2001 00477
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
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; ORGANISM: Homo sapiens
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; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-109-498-1

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Query Match      64.1%; Score 123; DB 15; Length 406;
Best Local Similarity 75.0%; Pred. No. 4e-13;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

```

```

Qy      1 ANGFLXXLRQGSILKRCXKXLCSPFXAXHIFRNXXRTROFWVSY 44
Db      1 ANAFLLXXLRPGSLKRCXKXQCSFXXARXIFKDAKRTLFWISY 44

```

```

RESULT 6
; Sequence 1, Application US/10255032
; Publication No. US20030100075A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030100075A10 No. US20030100075A1disk A/S
; TITLE OF INVENTION: HUMAN COAGULATION FACTOR VII POLYPEPTIDES
; FILE REFERENCE: 6357-WO
; CURRENT APPLICATION NUMBER: US/10/255,032
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: DK PA 2001 01413
; PRIOR FILING DATE: 2001-09-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT
; ORGANISM: human coagulation Factor VII
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)...(406)
; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid (gamma-carboxyglutamate)
US-10-255-032-1

```

```

Query Match      64.1%; Score 123; DB 15; Length 406;
Best Local Similarity 75.0%; Pred. No. 4e-13;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

```

```

Qy      1 ANGFLXXLRQGSILKRCXKXLCSPFXAXHIFRNXXRTROFWVSY 44
Db      1 ANAFLLXXLRPGSLKRCXKXQCSFXXARXIFKDAKRTLFWISY 44

```

```

RESULT 7
US-10-281-727-1
; Sequence 1, Application US/10281727
; Publication No. US20030130191A1
; GENERAL INFORMATION:
; APPLICANT: Petsson, Egon
; APPLICANT: Olsen, Ole Hvalsted
; TITLE OF INVENTION: Human Coagulation Factor VII
; FILE REFERENCE: 6410,200-US
; CURRENT APPLICATION NUMBER: US/10/281,727
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PA 2001 01627
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 60/335,383
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 406
; TYPE: PRT

```

```

; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Xaa means 4-carboxyglutamic acid
; OTHER INFORMATION: (gamma-carboxyglutamate)
US-10-281-727-1

```

```

Query Match      64.1%; Score 123; DB 16; Length 406;
Best Local Similarity 75.0%; Pred. No. 4e-13;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

```

```

Qy      1 ANGFLXXLRQGSILKRCXKXLCSPFXAXHIFRNXXRTROFWVSY 44
Db      1 ANAFLLXXLRPGSLKRCXKXQCSFXXARXIFKDAKRTLFWISY 44

```

```

RESULT 8
US-10-017-122-2
; Sequence 2, Application US/10017122
; Publication No. US20030087244A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MM1-007
; CURRENT APPLICATION NUMBER: US/10/017,122
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: 60/327,487
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-122-2

```

```

Query Match      64.1%; Score 123; DB 15; Length 466;
Best Local Similarity 52.3%; Pred. No. 4.6e-13;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

```

```

Qy      1 ANGFLXXLRQGSILKRCXKXLCSPFXAXHIFRNXXRTROFWVSY 44
Db      61 ANAFLEELRPGSLRCKEKEQCSFEAREIFKDAKRTLFWISY 104

```

```

RESULT 9
US-10-298-330-23
; Sequence 23, Application US/10298330
; Publication No. US20030100506A1
; GENERAL INFORMATION:
; APPLICANT: Nelissen, Gary L.
; TITLE OF INVENTION: Modified Vitamin K-Dependent
; FILE REFERENCE: 09531-127001
; CURRENT APPLICATION NUMBER: US/10/298,330
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/497,591
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/302,239
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 08/955,636
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 35
; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid
US-10-298-330-23

```

Query Match 54.2%; Score 104; DB 15; Length 40;  
Best Local Similarity 77.5%; Pred. No. 8.6e-11;  
Matches 31; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ANGFLXLRQGSILRXCRXXLCSFXXAHXIFRNXXRTROF 40  
Db 1 ANAFLLXLRQGSILRXCRXXLCSFXXAHXIFRNXXRTKLF 40

RESULT 10  
US-10-298-330-26  
; Sequence 26, Application US/10298330  
; Publication No. US20030100506A1  
; GENERAL INFORMATION:  
; APPLICANT: Nelsestuen, Gary L.  
; TITLE OF INVENTION: Modified Vitamin K-Dependent  
; FILE REFERENCE: 09531-127001  
; CURRENT APPLICATION NUMBER: US/10/298,330  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/497,591  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/302,239  
; PRIOR FILING DATE: 1999-04-29  
; PRIOR APPLICATION NUMBER: 08/955,636  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 33, 35  
; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid  
US-10-298-330-26

Query Match 53.1%; Score 102; DB 15; Length 40;  
Best Local Similarity 77.5%; Pred. No. 1.9e-10;  
Matches 31; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ANGFLXLRQGSILRXCRXXLCSFXXAHXIFRNXXRTROF 40  
Db 1 ANAFLLXLRQGSILRXCRXXLCSFXXAHXIFRNXXRTKLF 40

RESULT 11  
US-10-298-330-25  
; Sequence 25, Application US/10298330  
; Publication No. US20030100506A1  
; GENERAL INFORMATION:  
; APPLICANT: Nelsestuen, Gary L.  
; TITLE OF INVENTION: Modified Vitamin K-Dependent  
; FILE REFERENCE: 09531-127001  
; CURRENT APPLICATION NUMBER: US/10/298,330  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/497,591  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/302,239  
; PRIOR FILING DATE: 1999-04-29  
; PRIOR APPLICATION NUMBER: 08/955,636  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 25  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 32, 35

; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid  
US-10-298-330-25

Query Match 52.6%; Score 101; DB 15; Length 40;  
Best Local Similarity 77.5%; Pred. No. 2.8e-10;  
Matches 31; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ANGFLXLRQGSILRXCRXXLCSFXXAHXIFRNXXRTROF 40  
Db 1 ANAFLLXLRQGSILRXCRXXLCSFXXAHXIFRNXXRTKLF 40

RESULT 12  
US-10-298-330-22  
; Sequence 22, Application US/10298330  
; Publication No. US20030100506A1  
; GENERAL INFORMATION:  
; APPLICANT: Nelsestuen, Gary L.  
; TITLE OF INVENTION: Modified Vitamin K-Dependent  
; FILE REFERENCE: 09531-127001  
; CURRENT APPLICATION NUMBER: US/10/298,330  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/497,591  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/302,239  
; PRIOR FILING DATE: 1999-04-29  
; PRIOR APPLICATION NUMBER: 08/955,636  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 35  
; OTHER INFORMATION: Xaa = gamma carboxyglutamic acid  
US-10-298-330-22

Query Match 51.0%; Score 98; DB 15; Length 40;  
Best Local Similarity 75.0%; Pred. No. 9.3e-10;  
Matches 30; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ANGFLXLRQGSILRXCRXXLCSFXXAHXIFRNXXRTROF 40  
Db 1 ANAFLLXLRQGSILRXCRXXLCSFXXAHXIFRNXXRTKLF 40

RESULT 13  
US-10-298-330-2  
; Sequence 2, Application US/10298330  
; Publication No. US20030100506A1  
; GENERAL INFORMATION:  
; APPLICANT: Nelsestuen, Gary L.  
; TITLE OF INVENTION: Modified Vitamin K-Dependent  
; FILE REFERENCE: 09531-127001  
; CURRENT APPLICATION NUMBER: US/10/298,330  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: 09/497,591  
; PRIOR FILING DATE: 2000-02-03  
; PRIOR APPLICATION NUMBER: 09/302,239  
; PRIOR FILING DATE: 1999-04-29  
; PRIOR APPLICATION NUMBER: 08/955,636  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 44  
; TYPE: PRT  
; ORGANISM: Bos taurus

FEATURE: /  
NAME/KEY: VARIANT  
LOCATION: 6, 7, 14, 16, 19, 20, 23, 25, 26, 29, 35  
OTHER INFORMATION: Xaa = gamma carboxyglutamic acid or glutamic acid  
US-10-298-330-2

Query Match 50.5%; Score 97; DB 15; Length 44;  
Best Local Similarity 65.9%; Pred. No. 1.5e-09;  
Matches 29; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 ANGFLXXLRQSLXRCRXXCSPXXAHXIFRNXXRTROFV 44  
DB 1 ANSFLXXLRPGNVXRCXSVXCXFXAXXIFONTXDITAFWSFY 44

## RESULT 14

US-10-182-263-6  
Sequence 6, Application US/10182263  
Publication No. US20030022354A1  
GENERAL INFORMATION:  
APPLICANT: Jones, Bruce E  
APPLICANT: Gerlitz, Bryan E  
TITLE OF INVENTION: PROTEIN C DERIVATIVES  
FILE REFERENCE: X-13611  
CURRENT APPLICATION NUMBER: US/10/182,263  
CURRENT FILING DATE: 2002-07-22  
PRIOR APPLICATION NUMBER: 60/181948  
PRIOR FILING DATE: 2002-02-11  
PRIOR APPLICATION NUMBER: 60/189199  
PRIOR FILING DATE: 2000-03-14  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 419  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-182-263-6

Query Match 50.0%; Score 96; DB 15; Length 419;  
Best Local Similarity 48.8%; Pred. No. 1.9e-08;  
Matches 20; Conservative 2; Mismatches 19; Indels 0; Gaps 0;

QY 1 ANGFLXXLRQSLXRCRXXCSPXXAHXIFRNXXRTROFV 41  
DB 1 ANSFLXERLROGSLERECTIERICDPEBAKIFEDVDITLAFW 41

## RESULT 15

US-10-298-330-24  
Sequence 24, Application US/10298330  
Publication No. US20030100506A1  
GENERAL INFORMATION:  
APPLICANT: Nelsestuen, Gary L.  
TITLE OF INVENTION: Modified Vitamin K-Dependent  
FILE REFERENCE: 09531-127001  
CURRENT APPLICATION NUMBER: US/10/298,330  
CURRENT FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: 09/497,591  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/302,239  
PRIOR FILING DATE: 1999-04-29  
PRIOR APPLICATION NUMBER: 08/955,636  
PRIOR FILING DATE: 1997-10-23  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 24  
LENGTH: 40  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: MOD\_RES

LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29, 32, 35  
OTHER INFORMATION: Xaa = gamma carboxyglutamic acid  
US-10-298-330-24

Query Match 49.5%; Score 95; DB 15; Length 40;  
Best Local Similarity 75.0%; Pred. No. 3e-09;  
Matches 30; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 ANGFLXXLRQSLXRCRXXCSPXXAHXIFRNXXRTROF 40  
DB 1 ANAFLXXLRPGSLXRCXKXQCSFXAXXIFDXAKTKLF 40

Search completed: July 28, 2003, 12:38:59  
Job time : 32.5 secs

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## OM protein - protein search, using sw model

Run on: July 28, 2003, 12:22:40 ; Search time 20 Seconds  
(without alignments)  
93.084 Million cell updates/sec

Title: SEQ4

Perfect score: 192  
Sequence: 1 ANGFLXXLRGSLXRCRX...XXAHXIFRNXXRTQFWVSY 44

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	164	85.4	44	3	US-08-955-636-4
2	127	66.1	44	3	US-08-955-636-30
3	126	65.6	44	3	US-08-955-636-26
4	124	64.6	44	3	US-08-955-636-27
5	123	64.1	44	3	US-08-955-636-3
6	123	64.1	406	1	US-08-293-778-24
7	123	64.1	406	1	US-08-295-411-5
8	123	64.1	406	1	US-08-955-471-5
9	123	64.1	406	5	PCT-US92-10242-5
10	123	64.1	444	1	US-08-475-845-2
11	123	64.1	444	2	US-08-327-680-2
12	123	64.1	444	2	US-08-660-289-2
13	123	64.1	444	2	US-08-537-807-2
14	123	64.1	444	2	US-08-871-003-2
15	123	64.1	444	2	US-08-464-233-2
16	123	64.1	444	3	US-09-189-607-2
17	123	64.1	444	3	US-09-378-907-2
18	123	64.1	444	5	PCT-US94-05779-2
19	123	64.1	466	1	US-07-882-202A-4
20	123	64.1	466	1	US-08-021-615A-4
21	123	64.1	466	3	US-08-321-777-4
22	123	64.1	466	3	US-09-009-217-14
23	123	64.1	466	3	US-09-009-656-14
24	123	64.1	466	5	PCT-US93-04493-4
25	122	63.5	44	3	US-08-955-636-28
26	119	62.0	44	3	US-08-955-636-29
27	109	56.8	41	1	US-08-229-280-4

28	101	52.6	139	1	US-08-310-978-2	Sequence 2, Appli
29	101	52.6	139	1	US-08-474-042-2	Sequence 2, Appli
30	101	52.6	139	1	US-08-484-558-2	Sequence 2, Appli
31	101	52.6	139	1	US-08-774-592-2	Sequence 2, Appli
32	101	52.6	437	1	US-08-487-037-2	Sequence 2, Appli
33	101	52.6	437	1	US-08-487-037-3	Sequence 3, Appli
34	101	52.6	488	1	US-08-487-037-1	Sequence 1, Appli
35	98	51.0	44	3	US-08-955-636-23	Sequence 23, Appli
36	97	50.5	44	3	US-08-955-636-2	Sequence 2, Appli
37	96	50.0	44	3	US-08-955-636-24	Sequence 24, Appli
38	96	50.0	448	1	US-08-295-411-3	Sequence 3, Appli
39	96	50.0	448	2	US-08-955-471-3	Sequence 3, Appli
40	96	50.0	448	5	PCT-US92-10068-1	Sequence 1, Appli
41	96	50.0	448	5	PCT-US92-10242-3	Sequence 3, Appli
42	96	50.0	488	4	US-09-367-777-44	Sequence 44, Appli
43	96	50.0	488	4	US-09-367-791A-27	Sequence 27, Appli
44	95	49.5	487	1	US-08-469-486-53	Sequence 53, Appli
45	95	49.5	487	2	US-08-469-658-53	Sequence 53, Appli

## ALIGNMENTS

```
RESULT 1
US-08-955-636-4
: Sequence 4, Application US/08955636A
: Patent No. 6017882
: GENERAL INFORMATION:
: APPLICANT: Nelsaestuen, Gary
: TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
: FILE REFERENCE: 09531/002001
: CURRENT APPLICATION NUMBER: US/08/955.636A
: CURRENT FILING DATE: 1997-10-23
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 4
: LENGTH: 44
: TYPE: PRT
: ORGANISM: Bos taurus
: NAME/KEY: MOD RES
: LOCATION: (0)..(0)
: OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-4

Query Match      85.4%; Score 164; DB 3; Length 44;
Best Local Similarity 97.7%; Pred. No. 3e-22; 1; Indels 0; Gaps 0;
Matches 43; Conservative 0; Mismatches 1;

Cy      1 ANGFLXXLRGSLXRCRXLCGFXAHXIFRNXXRTQFWVSY 44
Db      1 ANGFLXXLRGSLXRCRXLCGFXAHXIFRNXXRTQFWVSY 44

RESULT 2
US-08-955-636-30
: Sequence 30, Application US/08955636A
: Patent No. 6017882
: GENERAL INFORMATION:
: APPLICANT: Nelsaestuen, Gary
: TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
: FILE REFERENCE: 09531/002001
: CURRENT APPLICATION NUMBER: US/08/955.636A
: CURRENT FILING DATE: 1997-10-23
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 30
: LENGTH: 44
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
```

```

; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-30
```

```
Query Match      66.1%; Score 127; DB 3; Length 44;
Best Local Similarity 77.3%; Pred. No. 1.2e-15;
Matches 34; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy      1 ANGFLLXLRQGLRXCRCXLCSPFXAXHIFRNXXRTROFWVS 44
Db      1 ANAFLLXLRQGLRXCRCXLCQCSFXXARXIFDAXRTKLFWISY 44
```

## RESULT 3

```
US-08-955-636-26
; Sequence 26, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-26
```

```
Query Match      65.6%; Score 126; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 1.8e-15;
Matches 33; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy      1 ANGFLLXLRQGLRXCRCXLCSPFXAXHIFRNXXRTROFWVS 44
Db      1 ANAFLLXLRQGLRXCRCXLCQCSFXXARXIFDAXRTKLFWISY 44
```

## RESULT 4

```
US-08-955-636-27
; Sequence 27, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-27
```

```
Query Match      64.6%; Score 124; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 4.1e-15;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy      1 ANGFLLXLRQGLRXCRCXLCSPFXAXHIFRNXXRTROFWVS 44
Db      1 ANAFLLXLRQGLRXCRCXLCQCSFXXARXIFDAXRTKLFWISY 44
```

```
RESULT 5
US-08-955-636-3
; Sequence 3, Application US/08955636A
; Patent No. 6017882
; GENERAL INFORMATION:
```

```
; APPLICANT: Nelsestuen, Gary
; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
; FILE REFERENCE: 09531/002001
; CURRENT APPLICATION NUMBER: US/08/955,636A
; CURRENT FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
US-08-955-636-3
```

```
Query Match      64.1%; Score 123; DB 3; Length 44;
Best Local Similarity 75.0%; Pred. No. 6.1e-15;
Matches 33; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy      1 ANGFLLXLRQGLRXCRCXLCSPFXAXHIFRNXXRTROFWVS 44
Db      1 ANAFLLXLRQGLRXCRCXLCQCSFXXARXIFDAXRTKLFWISY 44
```

## RESULT 6

```
US-08-293-778-24
; Sequence 24, Application US/08293778
; Patent No. 5580560
; GENERAL INFORMATION:
; APPLICANT: Nicolaisen, Else M.
; APPLICANT: Bjorn, Soren E.
; APPLICANT: Wiiberg, Finn C.
; APPLICANT: Woodbury, Richard
; TITLE OF INVENTION: MODIFIED FACTOR VII/VIII
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 55805600 No. 5580560disk of No. 5580560th America, Inc.
; STREET: 405 Lexington Avenue, 62nd floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,778
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,509
; FILING DATE:
; APPLICATION NUMBER: DK 3235/87
; FILING DATE: 25-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/434,149
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: PCT/DK88/00103  
FILING DATE: 24-JUN-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/898,248  
FILING DATE: 12-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Agis, Cheryl H.  
REGISTRATION NUMBER: 34,086  
REFERENCE/DOCKET NUMBER: 3129,224-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-867-0298  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-293-778-24

Query Match 64.1%; Score 123; DB 1; Length 406;  
Best Local Similarity 52.3%; Pred. No. 6.3e-14;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRQSLRXCRXXLCSFXAXHIFRNXXRTROFVSY 44  
Db 1 ANAFLELRPGSLRCKRYCCSFYATYATFKDAERTKLTWISY 44

RESULT 7  
US-08-295-411-5  
Sequence 5, Application US/08295411

GENERAL INFORMATION:  
APPLICANT: Griffin, John H.  
APPLICANT: Mesters, Rolf M.  
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
TITLE OF INVENTION: for Inhibiting Coagulation  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESS: Office of Patent Counsel, The Scripps  
ADDRESS: Research Institute  
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA

ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/295,411  
FILING DATE: 22-AUG-1994  
CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/793,989  
FILING DATE: 18-NOV-1991  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSR1263,0C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..152  
OTHER INFORMATION: /note= "Factor VII light Chain"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 153..406  
OTHER INFORMATION: /note= "Factor VII Heavy Chain"  
US-08-295-411-5

Query Match 64.1%; Score 123; DB 1; Length 406;  
Best Local Similarity 52.3%; Pred. No. 6.3e-14;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Oy 1 ANGFLXXLRQSLRXCRXXLCSFXAXHIFRNXXRTROFVSY 44  
Db 1 ANAFLELRPGSLRCKRYCCSFYATYATFKDAERTKLTWISY 44

RESULT 8  
US-08-955-471-5  
Sequence 5, Application US/08955471

GENERAL INFORMATION:  
APPLICANT: Griffin, John H.  
APPLICANT: Mesters, Rolf M.  
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
TITLE OF INVENTION: for Inhibiting Coagulation  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESS: Office of Patent Counsel, The Scripps  
ADDRESS: Research Institute  
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA

ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/955,471  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/295,411  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Fitting, Thomas  
REGISTRATION NUMBER: 34,163  
REFERENCE/DOCKET NUMBER: TSR1263,0C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-554-2937  
TELEFAX: 619-554-6312  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 406 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..152

OTHER INFORMATION: /note= "Factor VII Light Chain"  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 153..406  
 OTHER INFORMATION: /note= "Factor VII Heavy Chain"  
 US-08-955-471-5

Query Match 64.1%; Score 123; DB 2; Length 406;  
 Best Local Similarity 52.3%; Pred. No. 6.3e-14;  
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRQGSIXRCXKXLCSPFXAHXIFRNXXRTQFWVS 44  
 DB 1 ANAFLELRPGSLERCKEBCQCFEAREIFKDAERTKLFWISY 44

RESULT 9  
 PCT-US92-10242-5  
 Sequence 5, Application PC/TUS9210242

GENERAL INFORMATION:  
 APPLICANT: Giffen, John H.  
 APPLICANT: Meesters, Rolf  
 TITLE OF INVENTION: Serine Protease-Derived Polypeptides and  
 TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods  
 TITLE OF INVENTION: For Inhibiting Coagulation  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Office of Patent Counsel, The Scripps  
 STREET: 10666 North Torrey Pines Road, TPC 8  
 CITY: La Jolla  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 92037

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US92/10242  
 FILING DATE: 19921118

CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/793,989  
 FILING DATE: 18-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pitting, Thomas  
 REGISTRATION NUMBER: 34,163  
 REFERENCE/DOCKET NUMBER: SCRO472P  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 619-554-2937  
 TELEFAX: 619-554-6312  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 406 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 1..152  
 OTHER INFORMATION: /note= "Factor VII Light Chain"

NAME/KEY: Region  
 LOCATION: 153..406  
 OTHER INFORMATION: /note= "Factor VII Heavy Chain"  
 PCT-US92-10242-5

Query Match 64.1%; Score 123; DB 5; Length 406;  
 Best Local Similarity 52.3%; Pred. No. 6.3e-14;

Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;  
 QY 1 ANGFLXLRQGSIXRCXKXLCSPFXAHXIFRNXXRTQFWVS 44  
 DB 1 ANAFLELRPGSLERCKEBCQCFEAREIFKDAERTKLFWISY 44

RESULT 10  
 US-08-475-845-2  
 Sequence 2, Application US/08475845  
 Patent No. 5786955

GENERAL INFORMATION:  
 APPLICANT: Berkner, Kathleen L.  
 APPLICANT: Petersen, Lars C.  
 APPLICANT: Hart, Charles E.  
 APPLICANT: Hedner, Ulla  
 APPLICANT: Bregengaard, Claus  
 TITLE OF INVENTION: Modified Factor VII  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Townsend and Townsend Hourie and Crew  
 STREET: One Market Plaza, Steuart Street Tower  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: U.S.A.  
 ZIP: 94105-1492

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.24  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/475, 845  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/327,690  
 FILING DATE: 24-OCT-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/065,725  
 FILING DATE: 21-MAY-1993

CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/662,920  
 FILING DATE: 28-FEB-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Parmelee, Steven W.  
 REGISTRATION NUMBER: 31,990  
 REFERENCE/DOCKET NUMBER: 13952-8-4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 206-467-9600  
 TELEFAX: 415-843-5043  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 444 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-475-845-2

Query Match 64.1%; Score 123; DB 1; Length 444;  
 Best Local Similarity 52.3%; Pred. No. 6.9e-14;  
 Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRQGSIXRCXKXLCSPFXAHXIFRNXXRTQFWVS 44  
 DB 39 ANAFLELRPGSLERCKEBCQCFEAREIFKDAERTKLFWISY 82

RESULT 11  
 US-08-327-690-2

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Sequence 2, Application US/08327690
Patent No. 5817788
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Hourie and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,690
FILING DATE: 24-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-327-690-2

Query Match          64.1%; Score 123; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 6.9e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy      1 ANGFLXXLRQSLXKCRXXLCSPFXAHXIFRNXXRTROFWVS 44
Db      39 ANAFLELRPGSLERCEKCEQCFEAREIFKDAERTKLFWISY 82

RESULT 12
US-08-660-289-2
Sequence 2, Application US/08660289
Patent No. 5833982
GENERAL INFORMATION:
APPLICANT: Berkner, Kathleen L.
APPLICANT: Petersen, Lars C.
APPLICANT: Hart, Charles E.
APPLICANT: Hedner, Ulla
APPLICANT: Bregengaard, Claus
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Hourie and Crew
STREET: One Market Plaza, Steuart Street Tower
```

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CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,289
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/475,845
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/327,690
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/065,725
FILING DATE: 21-MAY-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/662,920
FILING DATE: 28-FEB-1991
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-8-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-289-2

Query Match          64.1%; Score 123; DB 2; Length 444;
Best Local Similarity 52.3%; Pred. No. 6.9e-14;
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

Qy      1 ANGFLXXLRQSLXKCRXXLCSPFXAHXIFRNXXRTROFWVS 44
Db      39 ANAFLELRPGSLERCEKCEQCFEAREIFKDAERTKLFWISY 82

RESULT 13
US-08-537-807-2
Sequence 2, Application US/08537807
Patent No. 5861374
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Modified Factor VII
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/537,807
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05779
FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 08/065,725
FILING DATE: 21-MAY-1993
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/662,920  
FILING DATE: 28-FEB-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-1DC  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-537-807-2

Query Match 64.1%; Score 123; DB 2; Length 444;  
Best Local Similarity 52.3%; Pred. No. 6,9e-14;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRQSLRXRCRXXLCSFXXAHXIFRNXXRTROFVSY 44  
DB 39 ANAFLEELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 14  
US-08-871-003-2  
Sequence 2, Application US/08871003  
Patent No. 5937864  
GENERAL INFORMATION:  
APPLICANT: Hart, Charles E.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hedner, Ulla  
APPLICANT: Rasmussen, Mirella E.  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zymogenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/871,003  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
CLASSIFICATION: 514  
NAME: Sawislak, Deborah A.  
REGISTRATION NUMBER: 37,438  
REFERENCE/DOCKET NUMBER: 90-07C7  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-871-003-2

Query Match 64.1%; Score 123; DB 2; Length 444;  
Best Local Similarity 52.3%; Pred. No. 6,9e-14;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRQSLRXRCRXXLCSFXXAHXIFRNXXRTROFVSY 44  
DB 39 ANAFLEELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

RESULT 15  
US-08-464-233-2  
Sequence 2, Application US/08464233  
Patent No. 6039944  
GENERAL INFORMATION:  
APPLICANT: Berkner, Kathleen L.  
APPLICANT: Petersen, Lars C.  
APPLICANT: Hart, Charles E.  
APPLICANT: Hedner, Ulla  
APPLICANT: Bregengaard, Claus  
TITLE OF INVENTION: Modified Factor VII  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart Street Tower  
CITY: San Francisco  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 94105-1492  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.24  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/464,233  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/327,690  
FILING DATE: 24-OCT-1994  
APPLICATION NUMBER: 08/065,725  
FILING DATE: 21-MAY-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/662,920  
FILING DATE: 28-FEB-1991  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Parmelee, Steven W.  
REGISTRATION NUMBER: 31,990  
REFERENCE/DOCKET NUMBER: 13952-8-3  
TELEPHONE: 206-467-9600  
TELEFAX: 415-543-5043  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-464-233-2

Query Match 64.1%; Score 123; DB 3; Length 444;  
Best Local Similarity 52.3%; Pred. No. 6,9e-14;  
Matches 23; Conservative 5; Mismatches 16; Indels 0; Gaps 0;

QY 1 ANGFLXLRQSLRXRCRXXLCSFXXAHXIFRNXXRTROFVSY 44  
DB 39 ANAFLEELRPGSLRECKEQCSFEAREIFKDAERTKLFWISY 82

Search completed: July 28, 2003, 12:28:21  
Job time : 20 secs